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US DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE

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TRANSMITTAL LETTER TO THE UNITED STATES  
DESIGNATED/ELECTED OFFICE (DO/EO/US)  
CONCERNING A FILING UNDER 35 U.S.C. §371

ATTORNEY DOCKET NUMBER  
2 PPT/PTO 1/78/USU.S. APPLICATION NO.  
(if known, enter 37 CFR 1.55)  
NEW 08/973363

International Application No.  
PCT/GB96/01341

International Filing Date  
June 5, 1996

Priority Date Claimed  
June 6, 1995

**Title of Invention**

AVIAN CHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN BIRDS

**Applicant(s) For DO/EO/US**

Richard GRIFFITHS and Bela TIWARI

Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:


1. ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C. §371.
2. ☐ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. §371.
3. ☐ This express request to begin national examination procedures (35 U.S.C. §371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. §371(b) and PCT Articles 22 and 39(1).
4. ☒ A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.
5. ☒ A copy of the International Application as filed (35 U.S.C. §371(c)(2))
  - a. ☒ is transmitted herewith (required only if not transmitted by the International Bureau). **ATTACHMENT A**
  - b. ☒ has been transmitted by the International Bureau.
  - c. ☐ is not required, as the application was filed in the United States Receiving Office (RO/US)
6. ☐ A translation of the International Application into English (35 U.S.C. §371(c)(2)).
7. ☐ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. §371(c)(3)).
  - a. ☐ are transmitted herewith (required only if not transmitted by the International Bureau).
  - b. ☐ have been transmitted by the International Bureau.
  - c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
  - d. ☐ have not been made and will not be made.
8. ☒ An unexecuted oath or declaration of the inventor(s) (35 U.S.C. §371(c)(4)). **ATTACHMENT B**
9. ☐ A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. §371(c)(5)).

**Items 10. to 13. below concern other document(s) or information included:**

10. ☒ An Information Disclosure Statement under 37 CFR 1.97 and 1.98. **ATTACHMENT C**
11. ☐ An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.
12. ☒ A **FIRST** preliminary amendment. **ATTACHMENT D**

☐ A **SECOND** or **SUBSEQUENT** preliminary amendment.
13. ☒ Other items or information: **FORMS PCT/IB/308 (2 PAGES) AND PCT/IPEA/409 (7 PAGES)**

COPY, FINANCE DEPT., USPTO  
CHARGE DEFICIENCIES  
TO DEPOSIT ACCT. # 23-0975

U.S. APPLICATION NO. (if known, see 37 CFR 1.5) NEW		INTERNATIONAL APPLICATION NO. PCT/GB96/01341		ATTORNEY'S DOCKET NO. 263/PPNTIR1172US	
14. <input checked="" type="checkbox"/> The following fees are submitted  <b>BASIC NATIONAL FEE (37 CFR 1.492(a)(1)-(5)):</b>  <input checked="" type="checkbox"/> Search Report has been prepared by the EPO or JPO..... \$ 930.00 <input type="checkbox"/> Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO..... \$1,070.00  <b>ENTER APPROPRIATE BASIC FEE AMOUNT =</b>				CALCULATIONS	PTO USE ONLY
Surcharge of \$130.00 for furnishing the oath or declaration later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492(e)).				\$	
Claims	Number Filed	Number Extra	Rate		
Total Claims	33 -20 =	13	X \$22.00	\$286.00	
Independent Claims	9 -3 =	6	X \$82.00	\$492.00	
Multiple dependent claim(s) (if applicable)			+ \$270.00	\$	
<b>TOTAL OF ABOVE CALCULATIONS =</b>				\$1,708.00	
Reduction by 1/2 for filing by small entity, if applicable. Verified Small Entity Statement must also be filed. (Note 37 CFR 1.9, 1.27, 1.28)				\$	
<b>SUBTOTAL =</b>				\$1,708.00	
Processing fee of \$130.00 for furnishing the English translation later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492(f)).			+	\$	
<b>TOTAL NATIONAL FEE =</b>				\$1,708.00	
Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). \$40 per property +				\$	
<b>TOTAL FEES ENCLOSED =</b>				\$1,708.00	
				Amount to be refunded	\$
				Amount to be charged	\$
a. <input checked="" type="checkbox"/> A check in the amount of <u>\$1,708.00</u> to cover the above fees is enclosed. A duplicate copy of this form is enclosed. b. <input type="checkbox"/> Please charge my Deposit Account No. 23-0975 in the amount of \$ _____ to cover the above fees. A duplicate copy of this sheet is enclosed. c. <input type="checkbox"/> The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. <u>23-0975</u> . A duplicate copy of this form is enclosed.					
<b>NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status.</b>					
SEND ALL CORRESPONDENCE TO:  WENDEROTH, LIND & PONACK 805 Fifteenth St., N.W., Ste. 700 Washington, D.C. 20005			<div style="text-align: center;">             SIGNATURE   <u>Warren M. Cheek, Jr.</u>            NAME   <u>33,367</u>            REGISTRATION NUMBER         </div>		
December 4, 1997			[ CHECK NO. <u>26460</u> ]		

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of :  
Richard GRIFFITHS et al. : ATTN: APPLICATION BRANCH  
Serial No. NEW :  
Filed December 4, 1997 : Attorney Docket No.  
263/PPNTIR1172US  
AVIAN CHD GENES AND THEIR USE IN  
METHODS FOR SEX IDENTIFICATION  
IN BIRDS

PRELIMINARY AMENDMENT

Assistant Commissioner for Patents,  
Washington, D.C.

Sir:

Prior to calculating the filing fee, please amend the above-identified application as follows:

IN THE CLAIMS

Please replace claims 1-32 consisting of pages 51-54 of the published international application papers with the substitute amended sheets consisting of pages 51-54 attached hereto containing claims 1-33.

Furthermore, to the claims 1-33 set forth in the amended sheets, please amend the claims as follows:

Claim 2, line 1, after "in" insert -- claim --.

Claim 5, line 1, delete "either of claims";

line 2, change "3 and 4" to -- claim 3 --.

Claim 10, line 2, delete "or claim 9".

Claim 11, line 1, delete "any";

line 2, change "one of claims 4, 9 and 10" to --  
claim 4 --.

Claim 12, line 1, delete "any";

line 2, change "one of claims 4, 9 and 10" to --  
claim 4 --.

Claim 13, line 1, delete "any";

line 2, change "one of claims 9 to 12" to -- claim  
9 --.

Claim 15, line 3, change "any one of claims 1 to" to --  
claim 1 --;

line 4, delete "14".

Claim 16, line 1, delete "any one";

line 2, change "of claims 1 to 14" to -- claim 1 -  
-.

Claim 17, line 2, delete "any";

line 3, change "one of claims 1-14" to -- claim 1  
--.

Claim 18, line 1, delete "any one";

line 2, change "of claims 1 to 14" to -- claim 1 -  
-.

Claim 22, line 2, change "claims 1-14" to -- claim 1 --.

Claim 23, line 3, delete "any";

line 4, change "one of claims 19-22" to -- claim  
19. --.

Claim 25, line 2, change "any one of claims 19-22" to -- claim 19 --.

Claim 27, line 2, delete in its entirety and replace with -- claim 19 --;

line 3, delete "claims 25 or 26".

Claim 28, line 2, change "any one of claims" to -- claim 1 - -;

line 3, delete "1 to 14".

Claim 31, line 2, delete "according to any one of";

line 3, delete "claims 1-14".

Claim 32, line 4, change "any one of claims 1 to 14" to -- claim 1 --.

#### IN THE ABSTRACT

Please insert the attached Abstract behind the figures of the application papers.

#### REMARKS

The present application papers consist of the published international application PCT/GB96/01341. An Abstract has been inserted in the application papers in conformance with U.S. practice corresponding to the Abstract of the international application. In addition, claims 1-32 of the published international application have been replaced with the substitute set of claims 1-33 submitted during prosecution of the international application. In addition, the substitute claims have been amended to eliminate the multiple dependency to reduce the PTO

filing fee. Favorable action on the merits is solicited.

Respectfully submitted,

Richard GRIFFITHS et al.

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December 4, 1997

## Abstract

The invention provides for DNA sequences (introns and exons) encoding two genes located on the Z and W chromosomes of birds. These genes can be used to identify the sex of most birds (Class Aves). In addition, the genes control the sex of the birds, a genetic process which is initiated as an embryo. Nucleic acid fragments, proteins, polypeptides, antibodies and related products and their use in medicine and agriculture are provided. The invention may be used in sex identification or for controlling the sex of adults or the progeny of commercially important animals.

2 Serial or Patent NO.:  
3 Filed or Issued:  
4 For: AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN BIRDS

VERIFIED STATEMENT (DECLARATION) CLAIMING SMALL ENTITY STATUS  
(37 CFR 1.9(f) and 1.27(c)) - SMALL BUSINESS CONCERN

I hereby declare that I am

- 5 ☐ the owner of the small business concern identified below:  
6 ☒ an official of the small business concern empowered to act on behalf of the concern identified below:

7 NAME OF CONCERN ISIS INNOVATION LIMITED  
ADDRESS OF CONCERN 2 South Parks Road, Oxford, OX1 3UB, United Kingdom.

I hereby declare that the above identified small business concern qualifies as a small business concern as defined in 13 CFR 121.3-18, and reproduced in 37 CFR 1.9(d), for purposes of paying reduced fees under section 41(a) and (b) of Title 35, United States Code, in that the number of employees of the concern, including those of its affiliates, does not exceed 500 persons. For purposes of this statement, (1) the number of employees of the business concern is the average over the previous fiscal year of the concern of the persons employed on a full-time, part-time or temporary basis during each of the pay periods of the fiscal year, and (2) concerns are affiliates of each other when either, directly or indirectly, one concern controls or has the power to control the other, or a third party or parties controls or has the power to control both.

I hereby declare that rights under contract or law have been conveyed to and remain with the small business concern identified above with regard to the invention, entitled

- 4 AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN BIRDS by inventor(s)  
1 RICHARD GRIFFITHS & BELA TIWARI  
described in

- 2,3 ☐ the specification filed herewith  
2,3 ☐ application serial no. \_\_\_\_\_, filed \_\_\_\_\_  
2,3 ☐ patent no. \_\_\_\_\_, issued \_\_\_\_\_

If the rights held by the above identified small business concern are not exclusive, each individual, concern or organization having rights to the invention is listed below\* and no rights to the invention are held by any person, other than the inventor, who could not qualify as a small business concern under 37 CFR 1.9(d) or by any concern which would not qualify as a small business concern under 37 CFR 1.9(d) or a nonprofit organization under 37 CFR 1.9(e). \*NOTE: Separate verified statements are required from each named person, concern or organization having rights to the invention averring to their status as small entities. (37 CFR 1.27)

- 8 NAME \_\_\_\_\_  
9 ADDRESS \_\_\_\_\_  
10 ☐ INDIVIDUAL ☐ SMALL BUSINESS CONCERN ☐ NONPROFIT ORGANIZATION  
11 NAME \_\_\_\_\_  
12 ADDRESS \_\_\_\_\_  
13 ☐ INDIVIDUAL ☐ SMALL BUSINESS CONCERN ☐ NONPROFIT ORGANIZATION

I acknowledge the duty to file, in this application or patent, notification of any change in status resulting in loss of entitlement to small entity status prior to paying, or at the time of paying, the earliest of the issue fee or any maintenance fee due after the date on which status as a small entity is no longer appropriate. (37 CFR 1.28(b))

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application, any patent issuing thereon, or any patent to which this verified statement is directed.

NAME OF PERSON SIGNING TIM COOK  
TITLE OF PERSON OTHER THAN OWNER Managing Director  
ADDRESS OF PERSON SIGNING 2 South Parks Road, Oxford, OX1 3UB, United Kingdom.

DATE 13/1/98



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Avian CHD genes and their use in methods for sex identification in birds

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### Introduction

The present invention relates to proteins, polypeptides, nucleic acid fragments, antibodies and related products and to their use in medicine and agriculture, for instance in diagnosis and therapy. More particularly the invention relates to a gene or genes which can be used to ascertain the sex of avian adults, embryos, cells, and tissues. These genes also control the sex of birds starting with action in the embryos and so control the sex of the progeny of birds

Much of our understanding of sex determination comes from three, extensively studied, model systems. In two of these, the fruitfly *Drosophila melanogaster* and the nematode *Caenorhabditis elegans*, it is the ratio of X chromosomes to autosomes that initiates sexual differentiation (Hodgkin 1992). In the mouse a single gene, *SRY*, located on the Y chromosome provides the impetus for male development; a pattern that is thought to be conserved throughout the mammals (Koopman *et al.* 1991 Foster, *et al.* 1992).

At the genetical level these three species employ very different molecular mechanisms, not only to control sex determination itself but to accommodate the differing dosages of genes that result from the males possessing a single X and the female two X chromosomes. These basic differences are largely due to the independent evolution of the three mechanisms and strongly suggests that other means of sex determination will have evolved elsewhere in the animal kingdom.

One class in which little is known about sex determination is the birds. They exhibit female heterogamety which means that the female

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has Z and W sex chromosomes and the male ZZ. This immediately suggests that sex determination in this class has an independent origin to that of their sister class, the mammals where it is the male that is heterogametic. Furthermore, it has been shown that whilst female  
5 mammals inactivate one of their X chromosomes as a method of dosage compensation (Grant & Chapman 1988), this does not seem to be a device employed by birds (Baverstock *et al.* 1982).

However, similarities do exist between the birds and mammals. The W chromosome, like the Y chromosome is usually smaller  
10 than its partner, and is also characteristically heterochromatic in appearance (Christidis 1990). The main exceptions to this rule are found in the 'primitive' representatives of both classes: the monotremes and the ratites where the morphological differences between the sex chromosomes are poorly defined (Graves 1987, Tagaki *et al.* 1972).

The heterochromatization of the W and Y results from the replacement of functional genetic loci with 'junk DNA' sequences. This process is thought to be a consequence of a suppression of recombination that has arisen to ensure that genes vital to the development of the heterogametic sex remain linked on the Y or W chromosome  
15 (Charlesworth 1991). As a result only a few genes such as *Ube1y* (Kay *et al.* 1991, Mitchell *et al.* 1991), *Zfy* (Page *et al.* 1987) and *SRY* itself remain on the mammalian Y chromosome. A similar situation is thought to prevail on the avian W chromosome where the presence of any functional genes has yet to be demonstrated, although it does possess vast arrays of  
20 repetitive elements (Griffiths & Holland 1990, Tone *et al.* 1982).

A further similarity in sex determination in birds and mammals is that the development of the male phenotype appears crucially dependent on the appearance of the testis. The female phenotype is the result of the 'default pathway'. For mammals this was first demonstrated  
25 by Jost (1947) who grafted an embryonic testis into genetically female

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rabbit embryos prior to sex determination. This was sufficient to allow the development of functional males. The same experiment has been carried out on chick embryos with comparable results (Stoll *et al.* 1978).

Once the testis has formed, the process of masculinization is adopted by the testicular hormones. The genetical switch that initiates testis determination is known to be *SRY* in mammals (Koopman *et al.* 1991). In birds, there appears to be no *SRY* homologue on the W chromosome (Griffiths 1991), although this is unsurprising given the separate evolution of sex determination in the two classes.

The only other pertinent evidence on the genetics of avian sex determination come from reports of chickens with abnormal chromosome complements. Table 1 shows data from Crew (1954) and McCarrey and Abbott (1979) on the phenotypes of the aneuploids so far described. These results suggest that the presence of the W chromosome in the aneuploid AA ZZW and the polyploid AAA ZZW has not acted as a dominant determinant of the female phenotype. This may mean that sex in birds may be determined more by the autosome to Z ratio, as in *Drosophila* and *C. elegans*. However, a ZO aneuploid which could confirm this hypothesis has yet to be described.

It must also be born in mind that XXY kangaroos, where *SRY* is thought to be the key male determining switch, exhibit both male and female characteristics (Graves 1987). This suggests that the limited aneuploid data that is available for birds should be interpreted with some caution.

To conclude, the genetic mechanism that controls sex determination in birds has not yet been elucidated. Here we suggest that a gene we have termed *CHD-W* (Chromodomain-*Helicase*-DNA binding on the W chromosome) alone or acting in conjunction with a closely related gene *CHD-1A* (Chromodomain-*Helicase*-DNA binding 1 Avian) initiates female development in birds.

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### The Invention

It is believed that all birds such as chickens and other species of commercial significance, will have two or more genes of the CHD type which will have a nucleotide sequence similar to the nucleotide sequences shown in Fig. 5, Fig. 7 and Fig. 8 and that the gene products will be proteins which are crucial to the determination of the sex of the organism. One of these genes will be located on the W chromosome and the other on an autosome or Z chromosome.

It will be understood that the exact sequence of the two genes will vary between species and between individuals of the same species at least at the nucleotide level and often also at the protein level. Complete or partial sequences of the chicken genes are shown in Fig. 5, Fig. 7 and Fig. 8. The gene or protein which contains sequence corresponding to those in Fig. 5, Fig. 7 and Fig. 8 will hereafter be referred to as an CHD-gene and proteins and fragments thereof, polypeptides, nucleic acids and fragments thereof and oligonucleotides containing part of a CHD gene will hereafter be referred to as CHD-proteins, CHD-nucleic acids and so on.

The present invention therefore provides a CHD-protein or a fragment thereof or polypeptide comprising a CHD-gene or a part thereof, subject to the proviso below.

The present invention also provides a protein or a fragment thereof or a polypeptide containing a mimetope of an epitope of a CHD-protein or fragment thereof of polypeptide containing a CHD-gene or a part thereof, subject to the proviso below. Such proteins, fragments and polypeptides are hereafter referred to as CHD-mimetope proteins or fragments thereof and CHD-mimetope polypeptides.

The present invention also provides a CHD-nucleic acid or a fragment thereof or oligonucleotide comprising a CHD-gene, or a part thereof subject to the proviso below.

In a particular aspect the present invention provides a single or double stranded nucleic acid comprising the CHD-gene of a bird or a part thereof of at least 17 contiguous nucleotide bases or base pairs, or a single or double stranded nucleic acid hybridizable with the CHD-gene of a bird, or part thereof of at least 17 contiguous nucleotide bases or base pairs, subject to the proviso below.

The invention further provides a nucleic acid or fragment thereof or an oligonucleotide encoding a CHD-protein or fragment thereof or a polypeptide comprising a CHD-gene or a part thereof or a CHD-mimotope protein or a fragment thereof or CHD-mimotope polypeptide, subject to the following proviso. These nucleic acids, fragments and oligonucleotides may have sequences differing from the sequences of CHD-nucleic acids, fragments and oligonucleotides due to alternative codon usage and/or encoding alternative amino acids sequences or mimetopes.

The present invention does not, however extend to any known protein or fragment thereof or polypeptide or nucleic acid or fragment thereof or oligonucleotide containing a CHD-gene related sequence such as the *Saccharomyces cerevisiae* SNF2/SWI2 gene, *Drosophila polycomb* and HP1 genes described below, insofar as that protein or fragment, polypeptide, nucleic acid or fragment or oligonucleotide is known *per se*.

The amino acid sequence of the CHD-gene has similarities to the chromobox and *Helicase* motifs of a number of discovered genes known to be involved in the remodelling of chromatin. This suggests that the CHD-protein of the present invention may have a regulatory function involving chromatin remodelling. However, none of these genes contain the chromobox and the *Helicase* of the CHD-gene which are conserved in conjunction, at least in the chicken, great tit, mouse and yeast but are not conserved in conjunction in the sequences of chromatin remodelling

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proteins not associated with sex determination at least at the stage of testis formation in birds. A gene that produces a protein having chromatin remodelling capacity but lacking these characteristic motifs is therefore outside the scope of the present invention.

5 In addition there are certain residues in the amino acid sequence of the chromobox and those residues immediately downstream thereof, of the CHD-gene which are also conserved at least between those found in the chicken, great tit, mouse and yeast but are not conserved in the sequences of chromatin remodelling proteins not associated with sex  
10 determination at least at the stage of testis formation in birds. Any one of these conserved residues is therefore considered characteristic of the CHD-gene proteins of the present invention. The characteristics of a CHD-chromobox will give a more complete and comprehensive description of the CHD-chromobox which can also be considered characteristic of the  
15 CHD-gene proteins of the present invention. A protein having chromatin remodelling capacity and a helicase motif but originating from a gene that lacks all or most of these characteristic amino acid residues in the chromobox motif is therefore outside the scope of the present invention.

The characteristic amino acids residues are shown in the  
20 alignment in Fig. 11, which is described in more detail below. When aligned with the illustrated sequences as shown, these residues fall at positions, 11,12, 20, 27, 34 inside the chromobox and 3, 6, 8, 12-15, 16 immediately downstream.

The nucleotide base sequence of the CHD-gene includes  
25 bases which encode the chromobox and *Helicase* motifs of chromatin remodelling proteins as described above. However, the base sequence of the CHD-nucleic acids of the gene will include codons specifying both or either chromobox and *Helicase* motifs and the former will have codons specifying one or more of the characteristic amino acid residues described  
30 above and/or will be hybridizable with a sequence that controls the sex

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determination of birds under conditions which substantially prevent hybridization to other sequences in birds that do not have these characteristics.

Preferably the CHD-nucleic acids of the invention encode a chromobox and a helicase and one or more, preferably all, of the characteristic chromobox amino acid residues and meet the above hybridization requirements.

Fragments of CHD-nucleic acids according to the present invention will likewise contain codons specifying the chromobox and helicase motifs or including at least part of either of these motifs or CHD-gene adjacent to the codons encoding these features and/or will be hybridizable with a sequence that controls the sex determination of birds under conditions which substantially prevent hybridization to other sequences in birds that do not have these characteristics.

Oligonucleotides containing the CHD-gene or a part thereof according to the present invention may contain codons specifying the chromobox or helicase motifs or including at least part of these motifs or CHD-gene but this is not essential. However all such oligonucleotides of the invention must be capable of hybridizing with a sequence or sequences that control the sex determination of birds or a gene intron, preferably under conditions which substantially prevent hybridization with any sequence not associated with sex determining sequence.

A sex determining sequence referred to herein is a sequence which contains the CHD-gene and which encodes a factor which when expressed at the appropriate stage and level during embryo development may result in testis formation and subsequent growth of the embryo as a male. It may alternatively refer to a sequence which encodes a factor which when expressed at the appropriate stage and level during embryo development prevents testis formation and results in the subsequent growth of the embryo as a female.

The hybridization conditions referred to above which prevent unwanted hybridization with sequences not associated with the sex determining gene will depend to some extent on the length of the nucleic acid, fragment or oligonucleotide of the invention tested. Thus for instance  
5 lower stringency will be sufficient to secure hybridization to sequences associated with the sex determining gene whilst preventing unwanted hybridization when the nucleic acid or fragments several thousand nucleotide base pairs in length than for a fragment of only a few hundreds of bases or an oligonucleotide of from 17 bases up to a few tens or  
10 hundreds of bases. With the smallest oligonucleotides and fragments of the invention hybridization conditions will be such that only complete complementarity between the oligonucleotide and or fragment and the sequences associated with the sex determining gene will result in hybridization.

15 Preferred nucleic acids and fragments of the invention will only hybridize selectively to the sequences associated with the sex determining gene or genes under conditions requiring at least 80%, for instance 85, 90 or even 95% more preferably 99% complementarity. Yet more preferred nucleic acids and fragments of the invention are those  
20 having a sequence corresponding exactly to that of those illustrated in Fig. 5, Fig. 7 and Fig. 8 although the nucleotide sequences may be longer or shorter than those illustrated and or may contain normally intronic sequences associated with these sequences

The invention particularly provides an oligonucleotide,  
25 polypeptide, nucleic acid or protein comprising the entire sequence of the CHD-gene of a bird and more preferably comprising the entire amino acid or nucleotide sequence of the chicken as set out in any one of Figs 1, 3, 5, 7, 8, 9, 10, 11.

The nucleic acids hybridizable with the CHD-gene of a bird  
30 are preferably hybridizable under moderate, or more preferably, high



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stringency conditions as defined below:

**Moderate stringency:**

Buffer: 2 x SSC  
5 Temp: 50°C  
Annealing period: 6-8hrs

**High stringency:**

Buffer: 1 x SSC  
10 Temp: 65°C  
annealing period: 6-8hrs

Moderate stringency as defined above corresponds with about 75% homology. High stringency as defined above corresponds with about 90% homology. 1 x SSC is 0.15 M sodium chloride, 0.015 M sodium citrate, pH 7.0.

Preferably the portion of the nucleic acid corresponding to or hybridizable with the CHD-gene is at least 20, more preferably at least 30, 40 or 60 and most preferably 100 or more nucleotide bases in length.

20 The nucleotide strands of the invention may be single or double stranded DNA or RNA. DNA's of the invention may comprise coding and/or non-coding sequences and/or transcriptional and or translational start and/or stop signals and/or regulatory, signal and/or control sequences such as promoters, enhancers and/or polyadenylation sites, endonuclease restriction sites and/or splice donor and/or acceptor, in addition to the CHD-gene sequence. Included within the DNA's of the invention are genomic DNA's and complementary DNA's (cDNA's) including functional genes or at least an exon containing the CHD-gene. They may also contain non-coding sequences such as one or more  
30 introns. Single stranded DNA may be the transcribed strand or the non-

transcribed (complementary) strand. The nucleic acids may be present in a vector, for instance a cloning or expression vector, such as a plasmid or cosmid or a viral genomic nucleic acid. RNA's of the invention include unprocessed and processed transcripts of DNA, messenger RNA (mRNA) containing the CHD-gene and anti-sense RNA containing a sequence complementary to the CHD-gene.

Nucleic acids of the present invention are particularly useful as primers for polymerase chain reactions (PCRs) conducted to ascertain the sex of a bird as defined below. They may also be used to express proteins or fragments or polypeptides corresponding to the whole or a part of a CHD-protein (whether or not containing a CHD-gene) or as probes in hybridization experiments. As used herein the term "fragments" used in connection with proteins is intended to refer to both chemically produced and recombinant portions of proteins.

The CHD-proteins and fragments thereof and polypeptides containing the CHD-gene or a part thereof and CHD-mimotope proteins and fragments thereof and CHD-mimotope polypeptides of the invention are useful in immunodiagnostic testing and for raising antibodies such as monoclonal antibodies for such uses. Antibodies against such proteins and fragments and polypeptides as well as fragments of such antibodies (which antibody fragments include at least one antigen binding site) including chemically derived and recombinant fragments of such antibodies, and cells, such as eukaryotic cells, for instance hybridomas and prokaryotic recombinant cells capable of expressing and, preferably secreting antibodies or fragments thereof against such proteins or fragments, also form part of the present invention.

The nucleic acids of the invention may be obtained by conventional means such as by the recovery from organisms using PCR technology or hybridization probes, by *de novo* synthesis or a combination thereof, by cloning the CHD-nucleic acids described below or a fragment

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thereof or by other techniques well known in the art of recombinant DNA technology.

Proteins and fragments thereof and polypeptides of the invention may be recovered from cells of organisms expressing a CHD-gene or generated by expression of a CHD-gene or coding sequence contained in a nucleic acid of the present invention in an appropriate expression system and host, or obtained by *de novo* synthesis or a combination thereof, by techniques well known in the art of recombinant DNA technology. The proteins, fragments thereof and polypeptides of the invention will contain naturally occurring L-a-amino acids and may also contain one or more non-naturally occurring a-amino acids having the D- or L- configuration

Antibodies may be obtained by immunization of a suitable host animal and recovery of the antibodies, by culture of antibody producing cells obtained from suitably immunized host animals or by *in vitro* stimulation of B-cells with a suitable CHD-protein, fragment or polypeptide or CHD-mimotope, protein, fragment or polypeptide and culture of the cells. Such cells may be immortalized as necessary for instance by fusion with myeloma cells. Antibody fragments may be obtained by well known chemical and biotechnological methods.

All these techniques are well known to practitioners of the arts of biotechnology. Reference may particularly be made to the well known text book "Molecular cloning: A laboratory manual" 2nd Edition (Eds Sambrook, J., Fritsch, E.F. and Maniatis, T.), (Cold Spring Harbour Laboratory, New York, 1989), hereafter referred to as "Maniatis".

The invention further provides the use of a nucleic acid, protein, polypeptide, antibody, or antibody producing cell as hereinbefore defined including the SNF2/SWI2, polycomb and HP1 or other chromobox or helicase containing protein for ascertaining the sex of a cell or organism of a bird or for isolating nucleic acids useful in ascertaining the sex of a bird

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and for instituting single sex breeding programmes.

Knowledge of the chicken or great tit sex determining gene or genes can be used to isolate the equivalent gene or genes from other birds. Once isolated from a particular species, this gene or genes and its sequence can typically be used in two types of application:

1. The construction of sequence based sexing tests which can be applied to embryos, tissues and other biological materials containing nucleic acids.
2. The genetic modification of the germ line of birds to create breeding systems that produce offspring statistically biased towards one sex or of one sex only (single sex breeding systems).

A particularly preferred technique for ascertaining the sex of a bird in accordance with the invention involves the use of an oligonucleotides as primers in a PCR, for instance as follows:

- 15 A cell or cells or remains thereof are obtained, for instance by surgical removal from an embryo or from the quill of a feather, and the DNA is released by a crude lysis procedure for instance using a detergent or by heating. Primer oligonucleotides of the invention are used to initiate a conventional PCR in order to amplify W chromosome linked CHD-related DNA from the cells. The products of the PCR are analysed by agarose gel electrophoresis and detected using labelled probes or by visual inspection. The presence of amplified CHD-W DNA indicates the presence of a CHD-W gene in the cells and thus, in birds, that the cell(s) were female. An example of a similar technique has been carried out by Griffiths & Tiwari (1995) on the Spix's Macaw (*Cyanopsitta spixii*). This is the world rarest bird (Guinness Book of Records) and DNA obtained from a moulted feather was sufficient to allow nested PCR amplification with CHD primers to show the bird was a male.
- 20
- 25

This technique may be applied for instance to identify the sex of embryos or adults for subsequent breeding programs in other bird

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species, or to control the sex of the progeny of breeding stock for commercial exploitation (by selection of the breeding stock or by slaughter or termination of animals of undesired sex).

The oligonucleotide primers for ascertaining or controlling sex  
5 in one species may also be used to ascertain or control sex in another species since hybridization of the primers to the CHD-gene of the other species will still serve to amplify the species-specific sequences.

Techniques for conducting such determinations are well known in the art of recombinant DNA technology.

10 In another aspect the present invention provides a process for isolating a W-chromosome specific sequence associated with the *CHD-W* gene of a bird which comprises probing a genomic library from a female of the species preferably of W chromosome sequences, for instance of lambda phage, cosmid or YAC library or cDNA library constructed from a  
15 tissue expressing the gene, with a probe comprising a nucleic acid, fragment or oligonucleotide of the invention as hereinbefore defined and a detectable label under high or moderate stringency.

Using the newly isolated subclone, Southern blots are performed on male and female DNA of the species of interest at high  
20 stringency to confirm that the correct clone has been isolated. The CHD-gene probe should give a female specific signal (other male/female shared bands may also be present at lesser intensities). The subclone is sequenced using standard methods and primers suitable for PCR chosen from the sequence so identified.

25 Alternatively, other approaches to cloning the sequences related to the sex determining gene could be used such as PCR methods using "degenerate" oligonucleotides. (For methods in PCR see, for example, "PCR Protocols - a Guide to Methods and Application"; edited by M.A. Innis, D.H. Gelfand, J.J. Sninsky, T.J. White; published by Academic  
30 Press, Inc.).

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Preferably the probe is CHD-1A or *CHD-W* or a fragment thereof or a nucleic acid or fragment or oligonucleotide having a sequence exactly as set out in Fig. 5, Fig. 7 or Fig. 8 for the chicken. Techniques for forming a genomic or cDNA library and for probing and detecting the detectable label and isolating the nucleic acid identified by the probe are well known in the art of biotechnology and recombinant DNA manipulation. The process may be conducted for instance using a probe having the chicken sequence such as the *CHD-W* sequence to identify and isolate the corresponding sequence from another bird such as Turkey. The thus-identified sequence can then be used to generate primers for PCR which in turn can be used to ascertain the sex of an individual or of cells, tissues, embryos or ovaries of the bird. This technique has been used by obtaining DNA from the Chicken and Hyacinth Macaw (*Anodorhynchus hyacinthinus*) to design primers for the Spix's Macaw (Griffiths & Tiwari 1995). This will permit experiments to ascertain sex to be conducted and controlled sex breeding of the bird as described below.

In addition, the nucleotide sequence of the CHD-genes are sufficiently conserved so that CHD primers can be designed that will allow PCR in a range of bird species. The primers P1, P2 and P3 shown in Figure 14 will allow CHD-W and CHD-1A amplification in a range of birds that allows sex to be identified.

The isolated nucleic acid, fragment or oligonucleotide may thereafter be amplified, cloned or sub-cloned as necessary. The invention further provides a process for detecting the sex of an individual bird or of cells, tissues, embryos, foetuses or ovaries or a bird, comprising conducting a polymerase chain reaction using DNA from the individual, cell, tissue, embryo or ovary as template and a nucleic acid, fragment or oligonucleotide of the invention as primer. Preferably the nucleic acid, fragment or oligonucleotide of the invention used as primer is *CHD-W* or *CHD-1A* or a part thereof and has a sequence corresponding exactly to the

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chicken sequence in Fig. 5, Fig. 7 or Fig. 8 or a part thereof or is a nucleic acid, fragment or oligonucleotide which is a W-chromosome specific sequence associated with the sex determining gene or genes of a bird of the same species as the individual cell, tissue, embryo, foetus or ovary  
5 whose sex is to be ascertained. The W-chromosome specific sequence associated with the sex determining gene or genes of the bird involved may itself have been obtained by the process of isolation and amplification or cloning described above. It can also be obtained by deduction from the sequence in Fig. 5, Fig. 7 or Fig. 8 or a sequence from another bird or  
10 animal.

The identification of the sex determining gene or genes according to the present invention raises the possibility of controlling the sex of progeny of commercially important animals such as chickens, turkeys and other avians. This will be valuable in many aspects of animal  
15 breeding and husbandry such as where one sex has more desirable characteristics, for instance only female progeny are desired for egg-laying breeds of chicken. The economic advantages of single sex breeding programmes and strategies for instituting these are described for instance in "Exploiting New Technologies in Animal Breeding; Genetic  
20 Developments", (Eds. Smith, C., King, J.Q.B. and McKay, J.C.), (Oxford University Press, Oxford, 1986).

The nucleic acids making up all or part of the sex determining gene, from the same or different animal species, can be introduced into any early embryo through established transgenic technology. This latter  
25 includes microinjection of DNA into pronuclei or nuclei of early embryos, the use of retroviral vectors with either early embryos or embryonic stem cells, or any transformation technique, (including microinjection, electroporation or carrier techniques) into embryonic stem cells or other cells able to give rise to functional germ cells. These procedures will allow  
30 the derivation of individual transgenic animals (founder transgenics) or

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chimeric animals composed in part of cells carrying the introduced DNA. Where the functional germ cells of the founder transgenic or chimeric animal carry the introduced DNA it will be possible to obtain transmission of the introduced DNA to offspring and to generate lines or strains of animals carrying these DNA sequences.

The nucleic acids making up part or all of the coding sequence of the sex determining gene, or derivatives of it, may be introduced in combination with its own regulatory sequences (promoter/enhancers etc.) or regulatory sequences from another gene, the whole making the "construct", to give expression from the construct at an appropriate developmental stage and tissue location critical to sex determination in the bird species under consideration. For example, in the chicken this would be between 6 and 7 days post lay.

15

### **Materials and Methods**

#### **Isolation of pGT-W, pGT1.7 and pGT8 Great Tit clones**

A great tit (*Parus major*) library was constructed from genomic DNA, partially restricted with *Mbol*, and the IFixII vector (Stratagene). The library was screened at high stringency with the 724bp probe (GT-W) cloned from a W chromosome specific polymerase chain reaction (PCR) product derived from the great tit (Griffiths & Tiwari 1993). Positive plaques were subject to two rounds of purification. Clone IGT2 contained an insert of 9.6kb that hybridized strongly to the probe sequence. The insert was subcloned as two *EcoRI* fragments of 1.7kb (pGT1.7) and 8kb (pGT8) into *EcoRI* cut pT7/T3 (Pharmacia).

#### **Isolation of CHD genes from the chicken**

Two chicken cDNA libraries were screened. The first was a mixed sex chick stage 10-12 cDNA library in IZapII which had been reamplified on 2



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occasions This library was provided by Dr I. J. Mason. The second library was constructed from mixed sex, 10 day chick mRNA. Total RNA was extracted using a guanidine thiocyanate based technique (Koopman 1993) and mRNA isolated using a Promega PolyATtract system 1000. A lZapII library was constructed using a Stratagene ZAP-cDNA synthesis kit. Plaques ( $2 \times 10^5$ ) from the stage 10-12 day library were screened at moderate stringency with a subcloned 433bp HindIII/SacI fragment from pGT8 that contained the 123bp region with identity to the mouse *CHD-1* gene (Delmas *et al.* 1993). A similar number of plaques from both libraries were screened with bases 428-4428 of *CHD-1A* (see Fig. 5 ). The 10 day library was also screened with bases 4059-5303 of *CHD-1A* (see Fig. 5). Positive plaques were purified prior to the excision of pBluescript plasmids and cloned inserts insert from lZapII using techniques recommended by Stratagene.

### Sequencing

All sequencing was carried out using the T7 DNA polymerase/7-deaza-dGTP chain termination sequencing kit from USB. All sequencing unless otherwise specified was carried out in both directions either by subcloning or through exonuclease III deletion with the Promega Erase-a-Base system.

### Southern Blot Analysis and Hybridization

Genomic DNA was extracted from blood (Griffiths & Holland 1990), digested with the appropriate restriction enzyme and Southern blotted onto Zeta-Probe GT under neutral conditions as described by the manufacturer (Bio-Rad). Prehybridizations and hybridizations were carried out in 0.25M  $\text{Na}_2\text{HPO}_4$ /5% SDS at either 65°C (high stringency) or 62°C (moderate stringency). Subsequent washes were carried out for a total of 1 hour in three changes of either 0.5 x SSC (75mM NaCl/7.5mM sodium

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citrate (pH7.5))/0.1%SDS at 65°C (high stringency) or 1 x SSC/0.1%SDS at 45°C (low stringency).

### Sex identification with PCR on dried and limited DNA in a

#### 5 Spix's Macaw

Stratagene provided a genomic Hyacinth Macaw Lambda  
FixII Library (Cat. No. 946402). Plaques were screened at moderate  
stringency with a 1.3Kb Chicken *CHD-W* subclone (spans 2670-4003  
nucleotides in the related Mouse CHD1 gene (Delmas *et al.*, 1993)). A  
10 *CHD-W* genomic fragment was isolated and aligned to the chicken and  
mouse homologues to allow the design and construction of 3 primers (5' to  
3') P3 AGATATTCCGGATCTGATAGTGA,  
P2 TCTGCATCGCTAAATCCTTT and  
P1 ATATTCTGGATCTGATAGTGA(C/T)TC.

- 15 DNA from the wild Spix's Macaw was extracted (Thomas &  
Pääbo 1993) from 1cm portions of the tips of 3 moulted flight feathers  
collected in 1994 and 1995. The negative extraction control was taken  
through an identical procedure. 1.5% of these extraction products or 50ng  
of genomic DNA from the reference samples were subject to semi-nested  
20 PCR. Primary amplification consisted of 20 cycles with primers P3 and P2;  
1% of the primary PCR product was subject to 30 cycles of amplification  
with P2 and P1. Samples were denatured for 1.5 min at 95°C then cycled  
between 57°C/30 sec, 72°C/15 sec and 94°C/30 sec with a 5 min final  
extension. Products were precipitated, cut with *DdeI*, reprecipitated and  
25 electrophoresed through visigel separation matrix (Stratagene). The  
accuracy of the test was confirmed using DNA from Spix's and Hyacinth  
Macaws of known sex (n=5 p=0.03). Uncut secondary PCR product from  
the wild bird was isolated (Dretzen *et al.* 1981), cloned using the  
Stratagene pCR-Script SK(+) kit and sequenced to confirm that the product  
30 had originated from a Spix's Macaw

### Sex identification with PCR in a variety of birds

DNA was isolated from blood taken from Chicken (5 individuals used), Marsh Harrier (28; *Circus aeruginosus*) and Kestrel (18 *Falco tinninculus*) all sexed by adult plumage, Bee-eater (4; *Merops* 5 *apiaster*, plumage/behaviour), Boobook Owl (2; *Ninox novaesiae*), White-faced Owl (2; *Ptilopsis leucotis*) Burrowing Owl (2; *Speotyto cumcularia*), Eurasian Eagle Owl (2; *Bubo bubo*), Long-eared Owl (2; *Asio otus*), Tawny Owl (3; *Strix aluco*, adult size), Starling (5; *Sturnus vulgaris*; Beak colour) and African Marsh Warbler (5; *Acrocephalus baeticatus*; reproductive 10 behaviour). DNA from a variety of parrots sexed by laparotomy was also used: Blue Fronted Amazon (3; *Amazona a aestiva*), Orange Winged Amazon (5; *Amazona amazonica*), Red Lored Amazon (3; *Amazona autumnalis*), Yellow Crowned Amazon (2; *Amazona o ochrocephala*), Tucamen Amazon (2; *Amazona tucamana*), Blue and Gold Macaw (6; *Ara* 15 *ararauna*), Citron Crested Cockatoo (2; *Cacatua sulphurea citronocristate*), Lesser patagonian (2; *Cyanolisous patagonus*), Blue Headed Pionus (1; *Pionus menstruus*), Plum Headed Parakeet (4; *Psittacula cyanocephala*), African Grey Parrot (12; *Psittacus erithacus*), Blue Throated Conure (2; *Pyrrhura cruentata*), Senegal Parrot (3; *Seneglus poicephalus*).

20 All the birds listed above were sexed from DNA using exactly the same PCR reaction. PCR reaction volumes of 20µl were made up of Promega Taq buffer (1x is 50mM KCl, 10mM Tris.HCl, 1.5mM MgCl<sub>2</sub>, 0.1% Triton X-100), 200µM of each dNTP, P2 (5'-TCTGCATCGCTAAATCCTTT) and P3 (5'- AGATATTCCGGATCTGATA) primers (approx 1µM), 50-200ng 25 of genomic DNA and 0.15 units of Taq polymerase. The thermal treatment was 94°C/1.5mins followed by 30 cycles of 55 or 56°C/15sec, 72°C/15sec, and 94°C/30sec with a finish of 56°C/1min and 72°C/5min. *HaeIII* (5 units; Promega) was used to cut 8ul of PCR product in 1x Promega restriction enzyme buffer 3 and 50ng/µl bovine serum albumin (Sigma) in a total 30 volume of 10µl. The digests and uncut PCR product were precipitated

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before being electrophoresed in a visigel (Stratagene) with ethidium bromide (40ng/ml) at 3.5V/cm.

### Results

5           The plasmid pGT-W contains a 724bp insert that hybridizes to a 4.9kb fragment only in the female great tit. Its DNA sequence was determined (Fig.1) and contains a 457bp open reading frame. A search of the EMBL DNA and protein sequence database found no significant matches. The sequence does contain a simple sequence consisting of a  
10   22bp run of thymidines.

          The pGT-W insert was used to probe Southern blots, at low stringency, of PvuII restricted genomic DNA of male and female great tit, starling, jackdaw (*Corvus monedula*), pied wagtail (*Motacilla alba*) and a species of new world flycatcher. These are species that cover the  
15   extremes of the passeriforme order according to the recent phylogeny of Sibley *et al.* (1988). In all but the jackdaw convincing hybridization to a single female specific fragment could be observed. In all species, hybridization to one or more non-sex specific fragments was also shown. A similar experiment was carried out with a non-passerine, the bee-eater  
20   (*Merops apiaster*), and this too resulted in faint hybridization to a female specific fragment and two, somewhat stronger bands, in both sexes.

          In order to further investigate the nature of the pGT-W insert we attempted to clone a larger fragment of genomic DNA which incorporated this motif. From around  $1.5 \times 10^5$  plaques from a great tit  
25   genomic library, two positives were obtained. After purification one of these gave superior hybridization and was investigated further. The 9.7kb insert was subcloned as pGT1.7 and pGT8 containing 1.7kb and 8 kb respectively. The pGT1.7 was sequenced in its entirety and approximately 2.8kb of the sequence of pGT8 was determined. Both were sequenced in  
30   a single direction. A 723bp region, starting 133bp from the 5' end of pGT8

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had a sequence that corresponded exactly to the pGT-W insert (Fig. 2).

The sequences derived from these subclones were used to search the EMBL database using the FASTA algorithms (GCG, Wisconsin package vers 7.3). A region of 123bp, starting 994bp from the 5' end of pGT8, showed a 79% nucleotide sequence identity to bases 3855-3977 of the mouse *CHD-1* gene (Fig. 3; Delmas *et al.* 1993). This corresponds to an 88% identity at the amino acid level.

Southern blots of *PvuII* digests of genomic DNA from male and female chicken and lesser black-backed gull (*Larus fuscus*) were probed at low stringency with a 433bp *SacI*/*HindIII* fragment of pGT8 that included the 123bp region with *CHD-1* identity (Fig. 4). Figure 12 shows that in the chicken hybridization was with a fragment of 3.1kb in the female only and with fragments of 1.5 and 6.0kb in both sexes. In the gull hybridization is similarly with a female specific fragment of 4.0kb a fragment of 3.0kb in males and females.

Delmas *et al.*, (1993) have already demonstrated the universal occurrence of the *CHD-1* in the mammals. The evidence this blot provides, which features species representing both the major divisions of the birds, suggests that a minimum of two types of CHD gene exist in this Class. The first we termed *CHD-W* to denote its W linkage. The 123bp region from the great tit would appear to be a short exon from this gene. The second hypothetical gene is closely related to *CHD-W* and we have it termed *CHD-1A*, where the A denotes its avian nature. This gene is either Z or autosomally linked as it occurs in both sexes.

### Isolation of *CHD-1A*

The *SacI*/*HindIII* great tit probe was used at low stringency to screen a lZap II cDNA library from stage 10-12 (33-49hrs after the appearance of the primitive streak) chicken embryos. A plating of  $2 \times 10^5$  plaques yielded a panel of 25 positive clones, 19 of these continued to

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hybridize intensely after purification. From three clones Z4, Z6 and Z11 a composite 6608 nucleotide sequence (Fig. 5) was determined using the strategy illustrated in Fig. 6.

The insert from the Z6 clone (bases 418-4426; Fig. 5) and a *Bgl*III (AGATCT) fragment of the Z4 clone (bases 4059-5303; Fig. 5) were used separately to screen a similar number of plaques from a second cDNA library constructed from 10 day old chicken embryos. This screening identified a total of 45 positives of which 16 were found to have sequence identity with the composite sequence derived from the first library. Two additional clones contained a closely related sequence that is dealt with below.

A proportion of the clones from both libraries show variation from the sequence given in Fig. 5 in one respect. Clones Z1, Z13, Z17, Z20 and Z23 are identical to the composite sequence 5' to base 4327 from there they terminate in an additional 37 to 163 bases of a new sequence that is identical in all five. Two clones from the second library CC43 and CC56 have 22 or 254bp of the same sequence at their 5' ends.

Downstream of this motif both clones regained homology with the composite sequence at base 4328 and show no further deviation from the original sequence. From these seven clones a composite 264bp sequence can be derived and this is illustrated in Fig. 7. None of the seven clones contain the whole of this sequence. Moreover, none of the ten clones that span the 4327/4328 insertion point contain any of this additional region. If inserted at this position, the motif has an in frame, open reading frame spanning its entire length. The motif is extremely adenosine rich and this makes the amino acid lysine extremely common in the putative translation (see Fig. 7). There are no splice donor or acceptor sites within the motif suggesting it is a final rather than an intermediary product of splicing.

Hybridization of a probe running from 2534 to 4428bp of the sequence chicken sequence to a blot of *Pvu*II cut, male and female

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chicken genomic DNA shows that hybridization occurs to fragments that are both W and autosomally or Z chromosomally located. The level of hybridization is significantly stronger to the fragments common to both sexes suggesting that the probe represents the *CHD-1A* gene.

5                *CHD-1A* is very closely related to the mouse *CHD-1* gene being 79.8% identical in a 5152nt overlap. At the amino acid level the identity is raised to 90% over 1750 residues. We do have an additional 1202bp of the 3' untranslated region but have not encountered a clone with an AATAAA termination signal or a 3' homopolymeric T tail. Both mouse  
10 and chicken sequences contain a stop codon in the same relative positions and sequence similarity is insignificant after this point. The published mouse sequence does not contain the additional 264bp motif described above.

                 The database search also identified an unpublished chicken  
15 derived sequence tagged as a delta crystallin binding protein (*DCBP*), with even greater identity than the mouse *CHD-1* gene: 99% over 2293 bp and 94% over 571 amino acid residues. The *DCBP* sequence is of 2292bp which extends over nucleotides 1922 to 4214 of *CHD-1A* (Fig. 5). Despite the high nucleotide sequence identity the region of amino acid similarity  
20 does not extend the full length of the *DCBP*. This is due to apparent deletions in the *DCBP* clone that provides an initiation methionine codon (257nt *DCBP*) and a stop codon (1939nt *DCBP*). The extremely high sequence identity, the fact that identity is maintained after the apparent stop in the *DCBP* sequence, that none of the 41 *CHD*-related clones we  
25 found have exact sequence identity and that only small sequencing mistakes would be required to introduce false stop and start codons suggests that the *DCBP* sequence is *CHD-1A* but has been sequenced slightly inaccurately. Further evidence is required to confirm this.

                 The database search with the whole *CHD-1A* gene also  
30 revealed significant identity to a previously unidentified portion of a 15 kb

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region of *S. cerevisiae* chromosome V. This region comprises an open reading frame of 4.4kb which lies between the RAD4 (Gietz & Prakash 1988) and the poly-A binding protein (Sachs *et al.* 1986) gene coding regions. In an overlap of 1538 amino acids, the whole of the yeast open  
5 reading frame, there is an identity of 37.7% and a similarity of 59% (Fig. 10). The degree of conservation this similarity implies suggests the yeast sequence encodes a homologue of *CHD-1A* that we shall term *CHD-1Y* for the sake of discussion.

Delmas *et al.*, (1993) identified four motifs in *CHD-1* with  
10 possible functional significance. *CHD-1A* retains such close homology to *CHD-1* that these regions are virtually unchanged and are likely to perform similar functions as they do in the mouse.

The first motif is a chromodomain (Paro & Hogness 1991) which falls between residues 274 and 311 (Fig. 9). Figure 11 compares  
15 the amino sequence of this region to that of eight others identified through a search of the EMBL database. The sequences fall into three categories. The first comprises the domain from *CHD-1*, *CHD-1A* and *CHD-1Y*. The second and third chromobox groups have been previously identified by (Pearce *et al.* 1992). The HP1 class comprises the *Drosophila* (James &  
20 Elgin 1986) and human (Saunders *et al.* 1993) HP1 genes and two murine modifier (*Mod*) genes (Singh *et al.* 1991). The HP1 class is characterized mainly by glutamic acid rich block of six residues upstream of the chromobox. The third group, the Pc class, comprises the *Drosophila Pc* gene (Paro & Hogness 1991) itself and its putative murine homologue the  
25 *Mod3* gene (Pearce *et al.* 1992).

A search of the EMBL data base with the *CHD-1A* putative helicase domain (residues 451-911, Fig. 9) raises the identity between this and *CHD-1Y* to 55% in an overlap of 471 amino acids. There is also  
30 significant, but lesser identity to, the putative helicase motifs in the human (Okabe *et al.* 1992), and *S. cerevisiae* (Laurent *et al.* 1992) *SNF2* gene,



human (Muchardt & Yaniv 1993) and *Drosophila Brahma* (Tamkun *et al.* 1992), *S. cerevisiae* *NPS1/STH1* (Laurent *et al.* 1992, Tsuchiya *et al.* 1992), human excision repair protein *ECCR6* (Troelstra *et al.* 1992) and the *RAD54* (Emery *et al.* 1991) and *MOT1* (Davis *et al.* 1992) genes of *S.*  
5 *cerevisiae*. It should be noted that none of these latter genes contain a chromobox.

Only the four CHD genes show significant homology to the third motif, a DNA binding region identified by Delmas *et al.*, (1993), whilst only *CHD-1A* and *CHD-1* have the three short basic HSDHR motif near the  
10 carboxy terminus, although this region is yet to be sequenced in *CHD-W*. The *CHD-1Y* gene apparently terminates before this point so does not share this motif. An extended discussion of the homology of the mouse *CHD-1* gene can be found in (Stokes & Perry 1995).

### 15 Isolation of *CHD-W*

Two, CC14 and CC4, of eight *CHD-1* related clones isolated from the 10 day chick embryo library using 349-4359nt of *CHD-1A* as a probe, overlap (Fig. 5) to provide the 1316bp of sequence given in Fig. 8. This is a sequence closely related to, but distinct from *CHD-1A*. Identity  
20 over the 1316bp overlap is 90.5% and 90.1% at the nucleotide and amino acid level respectively. An alignment of the putative translations of *CHD-1*, *CHD-1A* and *CHD-W* is given in Fig. 9. The amino acid identity between *CHD-1* and *CHD-1A* at 93.4% is marginally lower than that between that of *CHD-1* and *CHD-W*, 94.2%, over the same region

25 The 1335bp insert of CC4 was used at moderate stringency to probe a male/female, *PvuII* cut genomic blot featuring mouse, ostrich (*Struthio camelus*), chicken, bee-eater and hyacinth macaw (Fig. 13). Hybridization with the mouse and ostrich shows no evidence of any sex linkage, bands of the same size and equal intensity appearing in both  
30 sexes. Hybridization with the ostrich is particularly strong, greater even

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than with the cognate sequence in the chicken. This suggests that the genome size of the ostrich is considerably smaller than that of the chicken. It also demonstrates that the CHD genes cannot be used to sex the ostrich and, it is suggested, the other members of the ratites. There is no  
5 evidence from further work (reported later) that this effect should occur in other Parvclasses of the birds (Sibley *et al.* 1988).

In all the bird species apart from the ostrich, hybridization occurs with two types of fragment some that are female unique and others that are shared between the sexes. In the chicken some of the latter are of  
10 the same size as those hybridizing with the *CHD-1A* probe and result from cross hybridization under the conditions of low stringency that we employed. When probed with the CC4 sequence it is clear that hybridization with the female linked fragments is far stronger, at least in the chicken than with the shared fragments (bear in mind, also, that the female  
15 chicken only has a single dosage of the W linked gene). This indicates that CC4 is W linked and represents part of *CHD-W*.

The DNA contained in the Southern blot of the male and female chickens probed in Fig.13 contained identical amounts of DNA. However, examination shows that the shared bands are twice as strong in  
20 males (ZZ) as they are in females (WZ). The only way this could have happened is if the *CHD-1A* gene is Z linked. It is suggested this is the case in all birds.

#### 25 Sex identification with PCR on dried and limited DNA in a Spix's Macaw

The first test was devised to sex DNA extracted from the feathers of the last wild Spix's Macaw. This was the rarest bird on the planet and needed to be sexed so a mate could be selected from the 31 captive birds that remained. The test presented two problems. The first  
30 was extracting DNA from feathers the second providing a test that would

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work.

The procedure was published in Griffiths & Tiwari (1995) which covers the extraction of the DNA. The second test was to provide DNA from a Hyacinth Macaw which would yield data to allow construction of primers. A IFIX II library was provided by Stratagene and this was  
5 probed with the insert of the *CHD-1A* clone Z6 (-227-5302 Fig. 6) at moderate stringency. This provided 7 positive clones (A1, A2, A7, A8, A13, 1.2 and 5C). The inserts were extracted cut with *MboI* and subcloned into the *BamI* cut pUC18. This sublibrary was probed again with the Z6  
10 insert but this time at high stringency. The A12.3 subclone hybridized. This was sequenced and contained 111bp which is aligned to the chicken and mouse CHD genes in Fig 14. The similarity of this fragment to the chicken *CHD-W* suggested this was the Hyacinth Macaw homologue of the W chromosome located gene.

15 The data from A12.3 supplied information for the design of the primers required. It also provided evidence that the CHD sequences were sufficiently conserved in this region that a single set of primers could be designed to amplify both genes. Three primers, P1, P2 and P3, were designed to allow seminested PCR (Fig. 14). This technique allowed  
20 amplification of a 104bp region of both *CHD-W* and *CHD-1A* from DNA that was available from two captive Spix's Macaws of known sex. In each sex the PCR products were of the same size but sequence determination revealed that the *CHD-W* derived PCR product possessed a *DdeI* restriction enzyme site which was lacking in the *CHD-1A* product. Thus  
25 PCR amplification and *DdeI* cleavage of male Spix's Macaw DNA yields a only single product of 104 base pairs (bp), whilst from female DNA two products are apparent, one of 104bp and one of 73bp. The presence of the *CHD-1A* product in both sexes acts as a control to ensure the PCR amplification has been successful (Fig 15 & 16).

30 DNA was extracted from feathers moulted by the wild Spix's

Macaw using a technique devised for the purification of ancient DNA (Thomas & Pääbo 1993). The PCR-based test described above was used to demonstrate that *CHD-W* was not present in the sample (see Fig 16). This confirmed that the wild bird is male. A female Spix's macaw was released in March 1995 as a prospective mate.

### Sex identification with PCR on a variety of birds

Birds can be sexed from DNA by showing the presence (female: ZW) or absence (male: ZZ) of the female specific W chromosome.

At the molecular level this is carried out by the recognition of a W-linked marker. This can only be done after a W chromosome DNA marker is identified in the avian species. The test developed for the Spix's Macaw used *CHD-W* as a W linked marker. The data collected in designing this test suggested that this method may work to sex a variety of birds.

If the same test is to work on other bird species then two criteria must be met. The first is whether the PCR primers will amplify both *CHD* genes in other bird species. The Spix's Macaw test used the tiny amounts of DNA extracted from feathers so a seminested PCR was required. This used 3 primers which are aligned to the Mouse and Chicken *CHD* nucleotide sequences in Figure 14. The primer sites are highly conserved, there is no difference between the chicken genes and a solitary difference between the Mouse and Chicken in the 5' region of the P2 site. Theoretically, the primers should anneal to other bird species and, if a reasonable amount of DNA is available (>50ng), a single pair of primers should provide sufficient amplification.

A second requirement for the test is that the PCR products can be separated using a restriction endonuclease. In the Spix's Macaw the *DdeI* enzyme cuts *CHD-W* but not *CHD-1A*. Figure 14 shows that this discrimination would also occur in the Chicken. However, the *DdeI* cutting site CTNAG is not present in the *CHD-1A* of Spix's Macaw (CTNGG) nor

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the Chicken (CANAG) for different reasons. This suggests that the *DdeI* site is open to mutation so this form of discrimination is unlikely to be conserved. Other discriminatory sites are available: *DdeI* and *MaeII* sites are unique to *CHD-W* and the *HaeIII*, *MboII* and *XhoI* sites to *CHD-1A* and can be considered the first option. If these fail the *CHD-W* and *CHD-1A* PCR fragments can be cloned and sequenced so discriminatory sites can be discovered.

The theory we have presented suggests that a sexing test based on both avian *CHD* genes should work on many other bird species. Does this work in practice? The birds selected for trial are from across the avian class: Chicken (5 individuals), Marbled Murrelet (18), Kestrel (8), Marsh Harrier (28), Bee-eater (4), 1 pair of six species of Strigidae Owls from different genera (see Methods), Starling (5) and African Marsh Warbler (5).

The primers amplify a PCR product of the predicted size in all of the birds using primers P2 and P3 on 50-100ng of genomic DNA extracted from blood. Figure 17 illustrates this for 3 bird species but also includes amplification from human DNA. This shows that tests using P2 and P3 are open to human DNA contamination so appropriate precautions must be taken.

The *HaeIII* restriction enzyme cut the *CHD-1A* fragment alone in all 13 species (Fig 17) and, from the sequence data, would also have worked on the Spix's Macaw (Fig 16). Figure 17 shows that the *CHD-1A* in males is cut into two fragments (45bp, 59bp) which are not easily visible on the gel. In females *CHD-W* is uncut by *HaeIII* so remains at 104bp. The discrimination using *HaeIII* provided correct sex identification in all individuals.

### Discussion

#### The CHD genes

The female specific great tit probe GT-W was described by Griffiths and Tiwari (1993) as a means of identifying sex in this species.

5 The results presented here suggest this sequence represents part of a intron in a W linked gene. By moving downstream from this sequence it has been possible to isolate a putative exon from a gene that we have named *CHD-W* due to its close sequence identity to the mouse *CHD-1* gene (Delmas *et al.* 1993) and its W location.

10 Using the *CHD-W* fragment we attempted to isolate a similar, W linked sequence that Southern blot analysis had shown was present in the chicken. From several clones a 6606bp cDNA sequence was assembled but although it has close sequence identity to the great tit *CHD-W* fragment Southern blot analysis shows it is not located on the W chromosome. This second gene was termed *CHD-1A* (A = avian). This blot shows a second gene closely related to *CHD-1A* is W located. This sequence could not be cloned from a stage 10-12 chick cDNA library although 19 *CHD-1A* clones were isolated. However, two clones yielding 1347bp of a second CHD gene were isolated along with a further 14  
15 *CHD-1A* clones from a day 10 chick cDNA library. Southern blot analysis showed that this second clone was W chromosome derived and so represents *CHD-W*. Attempts are underway to isolate the remainder of *CHD-W*.

Southern blots of a variety of bird species showed that  
25 *CHD-W* is W chromosome linked in all birds except the ostrich. This suggests that the gene is sex linked throughout the class with the exception of the primitive ratites, which the ostrich represents, where it appears to be autosomally located.

An alternative explanation is that the *CHD-W* is in fact W  
30 linked in ratites but occurs in a region of the W chromosome which still

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recombines with the Z chromosome. If *CHD-1A* were Z linked, then recombination between Z and W linked copies of CHD would maintain their sequence identity resulting in the apparently autosomal location indicated by the Southern blot. A mammalian example would be the *MIC2* and *STS* genes that are located in the pseudoautosomal region of the Y chromosome (Ellis & Goodfellow 1989) and would give analogous results to those observed here.

Two lines of evidence support this alternative hypothesis. The first is that the Southern blot analysis suggests that *CHD-1A* is Z linked in non-ratites which would make the chromosomal location of the CHD-genes consistent throughout the class. Hybridization of *CHD-1A* to genomic blots is apparently stronger to fragments from male birds which would result from this sex having two copies of any Z linked gene in comparison to a single copy in the female (this result is not clear cut and requires confirmation by chromosomal *in situ*). The second line of evidence is that the sex chromosomes of the ratites are not morphologically differentiated as is the case with other birds (Christidis 1990). Morphological similarity suggests recombination still occurs between extensive regions of the ratite Z and W which may include the CHD genes and so produce the pattern of hybridization observed.

Although we have yet to clone the whole of *CHD-1A* the 6606bp sequenced so far shows a close identity to the mouse *CHD-1* gene over the putative coding region. It also includes all four features identified by Delmas *et al.* (1993) as having possible functional significance. This includes a chromodomain, a helicase, a DNA binding motif and a basic, five amino acid motif that is repeated three times (Fig. 9). The similarity of the sequence derived thus far from *CHD-W* to that of *CHD-1* and *CHD-1A* suggest it will be of similar length and possess these same motifs. We have also identified an alternatively spliced form of *CHD-1A* and *CHD-W* which has a similar adenine rich motif inserted at an identical point

(4327/4328nt *CHD-1A* and 1316nt *CHD-W*). The exact form of these alternative mRNAs is yet been elucidated. It is interesting to note that we obtained no clones that spanned these breakpoints which contained this additional motif; the sequence was built up from partial sequences derived  
5 from either 5' or 3' termini of different clones. Delmas *et al.*, (1993) produced a mRNA Northern blot probed with fragments of *CHD-1* occurring 5' to this breakpoint and discovered an mRNA species of about 4kb. This would correspond to a species cleaved near this insertion point. What purpose this would serve is unknown. Moreover the putative yeast  
10 homologue of *CHD*, *CHD-1Y*, which was identified from amino acid identity to *CHD-1A* from the genomic sequence on the EMBL database does not apparently have a similar motif. This is suggested because the *CHD-1Y* sequence was derived from a genomic clone which would allow the identification of any such sequence were it to be spliced in the normal  
15 manner.

The significance of the four functional domains found in the *CHD* genes will be discussed in turn. The first, the carboxy-terminal trimer repeat of five basic amino acid residues, has no known function and is not shared by any other sequences from the EMBL database. Furthermore,  
20 the *CHD-1Y* gene which is truncated by a little over 200 amino acid residues in comparison to *CHD-1* and *CHD-1A* does not contain this motif.

The second functional domain was identified by Delmas *et al.* (1993) as having sequence selective DNA binding capacity. Whether this is highly specific or just to A+T rich regions was not established. They  
25 also noted that this domain contains Lys-Arg-Pro-Lys-Lys and Arg-Gly-Arg-Pro-Arg motifs which enable genes like *HMG-1*, *D1* and *Engrailed* to bind in the minor groove of A+T rich DNA.

A third functional motif is located towards the N-terminus of the *CHD*-protein and is termed the chromodomain [Chromatin Organization  
30 Modifier; Paro, 1990 #459]. This is a highly conserved domain of between



37-50 amino acids that has been shown to be represented in the genomes of plants, nematodes, insects and vertebrates (Singh *et al.* 1991). Several chromobox genes have been isolated from human, mouse and *Drosophila* and have been divided into the *polycomb* (Pc) class and the

5 heterochromatin protein-1 (HP1) class on the basis of related structure (Pearce *et al.* 1992)). The CHD-genes have a distinct form of the chromobox characterized by close homology between yeast and vertebrate forms in the 5' half of the box itself but extending a further 17 residues downstream. These differences indicate that this form of the chromobox  
10 defines a third subgroup the CHD class

The *Pc* gene forms one of a eponymously named group (Pc-g) of about 12 genes defined through homeotic mutants in *Drosophila* that prevent fixation and maintenance of a determined state. They act as transcriptional repressors of homeotic genes, notably of the antennapedia  
15 complex (ANT-C; Paro, 1990). Members of the ANT-C and the other major group of *Drosophila* homeotic genes, the bithorax complex (BX-C), are responsible for defining segmental identity during development (Kaufman *et al.* 1980, Lewis 1978). Initially, their expression patterns are designated by early acting maternal and segmentation genes (see 4,6,7 Kennison).

20 However, these maternal genes are only transiently expressed. During the later stages of development their role as transcriptional activators is adopted by an assemblage of genes including the trithorax group (Trx-g), whilst many of their repressive effects are assumed by the Pc-g (Kennison 1993).

25 The *polycomb* (Pc) gene itself is perhaps the best studied member of the Pc-g. Zink and Paro (1989) used *Pc-B*-galactose fusion proteins to show that it binds to around 100 different sites on the polytene chromosome including loci where other members of the Pc-g are located. Any disruption of the chromodomain abolishes the specificity of this  
30 reaction (Messmer *et al.* 1992). However, the Pc-g protein appears to lack

any type of endogenous DNA binding capacity so it is thought that it acts as part of a protein complex with other components that are responsible for the site specific DNA binding (Paro 1990).

The repressive effects of the Pc-g are thought to be the result of chromatin compaction. In other words, the DNA is packaged into heterochromatin to prevent or reduce the expression of functional genes (Paro 1990). This is a mechanism related to position effect variegation (PEV; (Henikoff 1990)), to dosage compensation in mammals which sees the complete heterochromatization of one of the female's X chromosomes and possibly to gene imprinting whereby the expression of maternally and paternally inherited alleles differs (Peterson & Sapienza 1993). The links with PEV have recently been substantiated in that HP1, a recognized modifier of PEV, and *Pc* both contain chromodomains (Paro & Hogness 1991). Like the *Pc* protein, HP1 appears to form part of a structural complex that transforms euchromatin to heterochromatin. Furthermore, both PEV and the repressive effects of *Pc* are passed, in a clonal manner, to daughter cells ((Henikoff 1990, Struhl 1981); a characteristic also of gene imprinting.

With the CHD-type gene containing both a DNA binding motif and a chromobox it may appear reasonable to suggest that they encode repressors with an endogenous, site selective DNA binding system. However, CHD genes contain a further functional motif that is structurally related to the *Helicases*. The sequence identity is closest to the yeast *SNF2/SWI2* (Abrams *et al.* 1986) and *Drosophila Brahma* genes (Tamkun *et al.* 1992), both of which are transcriptional *activators*. Indeed, *Brahma* is part of the Trx-g which are considered direct antagonists to the Pc-g. Other genes which contain more distantly related *Helicase* domains are involved in DNA repair and chromatid separation during mitosis (Laurent *et al.* 1993, Sung *et al.* 1993).

The *SWI2* gene product has been shown to enhance the

transcription of other genes probably as part of a complex that includes *SWI1*, *SWI3*, *SNF5*, *SNF6* and in conjunction with gene specific DNA binding proteins (Laurent *et al.* 1991, Peterson & Heskowitz 1992). A mode of action strikingly similar to that of *Pc*.

5                   Although it remains to be formally demonstrated that *SWI2* is a helicase, it does have close structural similarities with proven *Helicase* genes and also possesses the required DNA stimulated ATPase activity (Laurent *et al.* 1993). Laurent *et al.*, go on to postulate that the *SWI2* containing complex may act by two mechanisms acting either separately or  
10                   in conjunction. In the first they envisage helicase mediated DNA melting to allow the egress of RNA polymerase II. Alternatively *SWI2* could allow chromatin remodelling, in effect overcoming any inhibitory packaging of the DNA and so enhancing transcription.

                  The juxtaposition of a *Helicase* and a chromodomain within  
15                   the same gene presents a paradox that may challenge the perceived roles of the two motifs. A simple explanation is that alternative splicing could remove one or other of these domains prior to translation. However, there is little support for this idea from the work of ourselves or Delmas *et al.*, (1993).

20                   An alternative explanation could be due to our lack of real knowledge about the function of the chromobox. Whilst it is well established that *Helicases* do disassociate DNA and so facilitate transcription (Matson & Kaiser-Rogers 1990), the role of the chromodomain in repression is based on more circumstantial evidence.  
25                   *Pc*, as we have seen, does not bind DNA itself although mutations in the chromobox prevent the formation of site specific complexes. It is possible that the chromodomain is involved more in maintaining the structural integrity of the repressive complex than in the repressive mechanism itself. Based on this supposition, the CHD-protein may form a different type of  
30                   complex able to bind at a site dictated or influenced by its own binding

domain and activate these loci via helicase activity.

While both this scenario is speculative it is probable that CHD-type genes are active during development and are able to bring about heritable changes in transcription. The presence of an endogenous DNA binding domain suggests it has fewer targets than *Pc*, for example, which could form part of several different active complexes. With *CHD-W* being confined to the W chromosome is likely to have a role in some aspect of female development and we suggest this may be critical to the determination of gender. In support this hypothesis we were unable to find any *CHD-W* clones in a library constructed prior to sex determination which occurs at day 7 (Lutz-Ostertag 1954) but were able to isolate two clones from a smaller pool of candidates at day 10. This suggests that the expression of *CHD-Y* may occur at a time consistent with its having a sex determining role.

If *CHD-W* alone or in conjunction with *CHD-1A* causes sex determination in birds then several potential mechanisms are plausible.

- (1) In the simplest scenario *CHD-Y* may act as a simple trigger like *SRY* (Koopman 1993) to either cause expression or repression of downstream genes in order initiate testis development.
- (2) *CHD-W* may interact with other autosomal or Z linked genes whereby the dosage of *CHD-W* in comparison these other factors causes initiates development down the male or female pathways.

A more complicated scenario is if *CHD-W* acts in together with *CHD-1A* to cause sexual differentiation. Different mechanisms could operate depending whether *CHD-1A* turns out to be Z linked as we suspect or autosomal.

- (3) If *CHD-1A* is Z linked, then male birds get two doses of the *CHD-1A* expression product to one in female birds. Perhaps the 1:1 ratio of functionally distinct *CHD-1A* and *CHD-W* products is what initiates female development whilst a double dosage of *CHD-1A* results in males.

(4) Alternatively, just the single dosage of Z linked *CHD-1A* product could result in female development and expression of *CHD-W* only occurs after sexual differentiation to equalize dosages of functionally similar proteins.

5 (5) If *CHD-1A* is autosomal however, it could be envisaged that *CHD-1A* and *CHD-W* are functional homologues and the three doses in females (AAW) is required to promote female development, whilst the double dosage in males (AA) causes the differentiation of the testis and the development of the male phenotype.

10 The evidence from aneuploid chickens discussed in the introduction, does suggest that the mechanism that does operate involves some degree of dosage dependence which tends to exclude mechanism (1). However the similarity of *CHD-W* to *HP1*, the *Pc* protein and other transcriptional modifiers that act through chromatin remodelling show that  
15 the expression of this type is crucially dependent on dosage (Locke *et al.* 1988) . With the different dosages of gene product and/or potential target sites that aneuploids possess it may be that analysis of these type of mutants has, thus far, served to confuse the issue.

## 20 Sex Identification

The first W-chromosome linked DNA was isolated by Tone *et al.* (1982) from the Chicken. Since then, a number of other W-linked avian sequences have been discovered (e.g. Griffiths, 1990; Rabenold, 1991; Griffiths, 1993). In all but one case, described later, these DNA fragments  
25 appear to be non-functional repeats. For instance, the related *XhoI* and *EcoRI* fragments in Chicken may comprise 70-90% of the W chromosome (Saitoh *et al.* 1991). This repeat and others in the Lesser Black-backed Gull (*Larus fuscus*) can be used to sex birds by the rapid dot blotting technique (Griffiths & Holland 1990). Other less repetitive W chromosome  
30 markers can be used to sex birds either by probing Southern blots

(Rabenold *et al.* 1991) or through the use of PCR (Griffiths & Tiwari 1993).

The major problem with all non-functional W-linked DNA is the speed with which they evolve. The chicken *XhoI* repeat is fairly typical. Through low stringency hybridization to a Southern blot it can be used to sex the Turkey (*Meleagris gallopavo*) and the Pheasant (*Phasianus versicolor*, Saitoh *et al.* 1991). These bird species are closely related to the Chicken by being members of the family Phasianidae. By contrast, the functional *CHD-W* region described here is 96% (3/67 Fig 3) identical between Chicken and Spix's Macaw and this only drops to 86% between the Chicken *CHD-W* and the Mouse *CHD1* (15/110 Fig 3). This level of conservation means that the chicken *CHD-W* probe can be used on Southern blots to sex birds from all over the class Aves.

The only exception to the non-functional avian W-linked sequences is *DZWM1* which is a putative gene, cloned from a cDNA turkey library. Like *CHD-W* this gene appears to be sex linked in many bird species. Unfortunately, so little information has been published in the papers that describe *DZWM1* that the nature of the gene remains unknown (Dvorák *et al.* 1992, Halverson 1990, Halverson & Dvorák 1993).

For sexing large numbers of birds Southern blot analysis is slow and expensive. The technique that we have used is based on a PCR using P2 and P3 primers followed by a *HaeIII* digestion of the of the amplified product. The digestion distinguishes between the *CHD-W* product which is uncut and the *CHD-1A* which is cut. The technique will work to sex a range of bird species that span the class Aves. The primers target a highly conserved region so are likely to be 'universal' to the birds but the discriminatory *HaeIII* site which cuts *CHD-1A* but not *CHD-W* shows no real reason to be conserved. If *HaeIII* does fail to be discriminatory other cutting sites have been suggested or the *CHD-W* and *CHD-1A* PCR products can easily be sequenced to look for an alternative. Alternatively, the different nucleotide sequence of the amplified *CHD-W*

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and *CHD-1A* suggests that the two PCR products would be separable on an agarose gel of around 3% or a non-denaturing acrylamide gel. This would remove the need for a cutting enzyme and may well make the sexing technique more easy to use.

5           The CHD based test appears to be fairly solid but the chances of a peculiar mutation in some bird species is not impossible. Cases concerning *SRY/Sox3* genes on the sex chromosomes in mammals supports this claim. In two species of the vole *Ellobius* males have neither a Y chromosome nor an *SRY* gene (Just *et al.* 1995). In a second case,  
10       four species of *Akodon*, the Mole Vole, have 15-40% of fertile females with XY chromosomes and an *SRY* gene (Bianchi *et al.* 1993). These examples are particularly peculiar in that the *SRY* gene is accepted as the gene that determines sex throughout the mammals. In neither case would the detection of *SRY* reliably inform you of the animals sex.

15           These examples from the Muridae may never occur with the CHD genes of birds. However, it does suggest that sex identification by the amplification of *CHD-W* and *CHD-NW* should always be validated by a test on several individuals in a new species before it is applied. Despite this warning, the use of the test described here or by other means using  
20       the *CHD-W* or *CHD1A*, these genes provide a method to sex most bird species.

25

30

**Table 1.** Sex of domestic fowl with normal and abnormal chromosome complements (from McCarrey & Abbott (1979) and Crew (1954)).

Chromosome complement	Phenotype
AAZZ	Male
AAZW	Female
AAZZW	Male?
AAZZZ	Male
AAAZZZ	Male
AAAZZW	Intersex/male

### Figure Legends

Figure 1. The DNA sequence of the pGT-W insert.

Figure 2. A map of the 9.6kb insert of the IFixII clone isolated from the great tit using pGT-W. pGT1.7 and pGT8 are the two *EcoRI* subclones into which the fragment was divided. The broken line corresponds to the region with absolute sequence identity to the pGT-W insert. The position of the region with identity to the mouse *CHD-1* gene is indicated.

Figure 3. An alignment of 123bp fragment of the great tit (GT) *CHD-W* gene in pGT8 with the autosomal/Z located chicken (C) *CHD-1A* the chicken *CHD-W* gene and bases 3855-3977 of the mouse (M) *CHD-1* gene. An alignment of the deduced amino acid sequence is also given.

Figure 4. The section of pGT8 that hybridized to a female specific fragment of 3.1kb in the chicken. This probe was also used to screen the chicken cDNA library. The hatched line represents the female specific great tit motif shown in Fig. 3.

(2)?



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Figure 5. The complete nucleotide sequence of CHD-1A as defined by the clones Z4, Z6 and Z11. Two asterisks underlie the position where part of the sequence illustrated in Fig7 is spliced onto the 5' or 3' ends of a proportion of the clones isolated. The ATG at nucleotide 228 is the start codon whilst TAA at 5388 is the stop codon.

Figure 6. The strategies used to determine the nucleotide sequence of *CHD-1A* and *CHD-W* given in Fig. 5 and Fig. 8. The top line represents the mouse clone given by (Delmas et al. 1993). The three 'Z' clones of *CHD-1A* and the 'CC4' and 'CC14' clones of *CHD-W* were derived from either a stage 10-12 or a 10 day chick cDNA library respectively. Arrows indicate the direction of sequence determination. Note Z6 actually ran from -227 to 69. These nucleotides were determined and are found in Fig 5

Figure 7. A composite nucleotide sequence and putative translation of the motif that is found spliced to a proportion of the 5' or 3' termini of *CHD-1* clones or the 3' end of the *CHD-W* clone CC14. The portion attached to the CC14 sequence is incomplete.

Figure 8. A partial nucleotide sequence of *CHD-W* as defined by the clones CC4 and CC14.

Figure 9. An alignment of the deduced amino acid sequences of the chicken (C) *CHD-1A* and *CHD-W* with the mouse (M) *CHD-1*. With gaps introduced to maximize alignment they show a sequence identity of 91.6% over 1365 residues. The \$ sign indicates start and stop codons. Boxed sections are the chromodomain (C), Helicase (H), and the region containing the DNA binding domain (B) identified by Delmas et al., (1993). A trimer repeat of a basic HSDHR motif is underlined. A\* denotes residue identity and . similarity.

Figure 10. An alignment of the deduced amino acid sequences of *CHD-1A* and *CHD-1Y* a putative yeast homologue of the chicken gene identified through a search of the EMBL data base. With

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gaps introduced to maximize alignment they show a sequence identity of 37.7% over 1538 residues. | indicates identity and : conservative substitution.

Figure 11. Comparison of 9 chromodomain sequences.

- 5 Vertical lines indicate the extent of the chromodomain as defined by Paro & Hogness (1991). The top three sequences represent the CHD class of chromodomain to add to the HP1 class and Pc class][;-l08k9ouygytrdevz as defined by Pearce et al. (1992). The first letter of each annotation indicates the animal of origin: C, chicken; M mouse; D, Drosophila; H, human; Y, *S. cerevisiae* whilst the remainder identifies the gene type. The yeast gene is a possible CHD homologue identified by its close identity to the vertebrate forms. \* indicates sequence identity within the groups and ^ identity between all nine sequences. \_ indicate amino acid residues inside and downstream of the motif that are characteristic of the CHD class chromobox.
- 10
- 15

Figure 12. Genomic Southern blots of DNA from male and female chickens and lesser black-backed gulls digested with PvuII and probed with a 433bp HindIII/Sac fragment of pGT8 (Fig 4.) at moderate stringency. Hybridization with female linked fragments and fragments common to both sexes can be observed in both species. Numbers give approximate sizes in kilobases.

20

Figure 13. Genomic Southern blots of DNA from male (M) and female (F) mice, ostrich, chicken, bee-eater and hyacinth macaw probed with the 1335bp insert of CC4 at moderate stringency.

- 25 Hybridization with mouse and ostrich is with fragments shared by both sexes whilst the non-ratite birds show additional hybridization to female specific fragments. In these latter species, the signal from female linked hybrids is stronger than with autosomal/Z linked fragments indicating that the probe is derived from the W chromosome. Numbers give approximate sizes in kilobases.
- 30

Figure 14. The nucleotide sequence of part of a single CHD1 gene isolated from the Mouse and the homologous genes from the Chicken, Hyacinth (A12.3 subclone) and Spix's Macaw all arranged as putative codons. Dashes denote nucleotides shared with the Mouse  
 5 sequence. The primers designed are shown on the diagram. An arrow head indicates a non-synonymous mutation in the Spix CHD-W. The *DdeI* (CTNAG) and *HaeIII* (GGCC) sites are underlined.

Figure 15. The technique of PCR sex identification in the Spix's Macaw. Semi-nested PCR amplification is carried out on both sexes  
 10 with the primers P2/P3 then P1/P2 to provide products of identical sizes in both sexes. The products are then cut with restriction enzyme *DdeI* which cuts only the CHD-W product from the female. The cut products are run on a visigel and the difference between the sexes can be visually detected. See Fig 17 for an example.

15 Figure 16. *DdeI* restricted PCR products demonstrating that remaining wild Spix's Macaw is male. Lane 1. the wild bird 2. negative extraction control 3. known male 4. known female. The larger fragment is of 104 bp and the female W-chromosome specific fragment of 73 bp.

Figure 17. Sex identification in the Marsh Harrier (MH),  
 20 Chicken (C) and African Marsh Warbler (AMW) carried out using an identical reaction. For each species genomic DNA of male and female birds was subject to PCR with primers P2 and P3 and the product of 110bp is visible in lanes 1 and 2. In lane 3 the entire male PCR product, amplified from *CHD-1A*, has cut into two parts with *HaeIII* (65bp, 45bp). In females,  
 25 lane 4 this *HaeIII* cut product is also present but the *CHD-W* product remains uncut so the sex can be identified. The 'Kb' lane contains a '1Kb DNA ladder' (BRL), the 'H' lane is PCR reaction with P2 and P3 carried out on human genomic DNA and -ve lane contains a negative PCR reaction.

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CLAIMS

1. The nucleotide sequences of CHD-1A and CHD-W as shown in Fig. 5, Fig. 7 and Fig. 8.
2. A clone or subclones of CHD-1A and CHD-W as defined in 1.
3. A fragment of CHD-1A and CHD-W, as shown in Figure 5, Figure 7 and Figure 8, capable of giving W specific signal on hybridization to genomic DNA of a non-ratite bird.
4. A fragment of CHD-1A and CHD-W, as shown in Figure 5, Figure 7 and Figure 8, obtainable by restriction endonuclease digestion thereof and being capable of giving a W specific signal on hybridization to genomic DNA of a non-ratite bird.
5. A clone or subclone of a fragment according to either of claims 3 and 4.
6. A nucleic acid or fragment or oligonucleotide having substantially the sequence of CHD-1A and CHD-W as set out in Fig. 5, Fig. 7 and Fig 8.
7. A clone or a subclone of a nucleic acid or fragment or oligonucleotide according to claim 6.
8. A nucleic acid or fragment or oligonucleotide having substantially the same sequence of the chicken or great tit CHD-gene as set out in Figs 1, 3, 5, 7 or 8.
9. A nucleic acid or fragment or oligonucleotide containing substantially the nucleotide sequence set out in Figure 5, Figure 7 or Figure 8, being capable of giving a W chromosome specific signal on hybridization to the genomic DNA of a non-ratite bird.
10. A nucleic acid or fragment or oligonucleotide according to claim 4 or claim 9 capable of giving W chromosome specific signal on hybridization to the genomic DNA of a chicken, turkey, duck, parrot.

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11. A nucleic acid or fragment or oligonucleotide according to any one of claims 4, 9 and 10 capable of giving W chromosome specific signal on hybridization to the genomic DNA of a non-ratite bird under conditions of high stringency.
12. A nucleic acid or fragment or oligonucleotide according to any one of claims 4, 9 and 10 capable of giving W chromosome specific signal on hybridization to the genomic DNA of a non-ratite bird under conditions of low stringency.
13. A nucleic acid or fragment or oligonucleotide according to any one of the claims 9 to 12 containing substantially the sequence of the chicken CHD-gene as set out in Fig. 5, Fig. 7 and Fig. 8.
14. A nucleic acid or fragment or oligonucleotide, containing substantially the nucleotide sequence shown in Figure 5, Figure 7 or Figure 8, encoding a CHD-protein, fragment thereof or polypeptide containing a CHD-gene or part thereof or encoding a CHD-mimotope protein or fragment thereof or CHD-mimotope polypeptide.
15. A process for ascertaining the sex of a non-ratite bird or of an embryo, foetus, cell or tissue of a non-ratite bird comprising hybridizing a nucleic acid or fragment or oligonucleotide according to any one of claims 1 to 14 with DNA or RNA of the non-ratite bird or the embryo, foetus, cell or tissue or with cDNA reverse transcribed from RNA of the non-ratite bird or the embryo, foetus, cell or tissue or with cDNA or DNA amplified by cloning or polymerase chain reaction from DNA or RNA of the non-ratite bird or the embryo, foetus, cell or tissue.
16. Use of a nucleic acid or fragment or oligonucleotide of any one of claims 1 to 14 in ascertaining the sex of a non-ratite bird or of an embryo, foetus, cell or tissue of a non-ratite bird.
17. A process for controlling the sex of the progeny of a non-ratite bird comprising inserting a nucleic acid or fragment or oligonucleotide of any

AMENDED SHEET

one of claims 1-14 into the genome of the non-ratite\_bird or progenitor thereof.

18. Use of a nucleic acid or fragment or oligonucleotide of any one of claims 1 to 14 in controlling the sex of the progeny of a non-ratite bird.
19. An avian CHD-protein, fragment thereof or polypeptide containing a CHD-gene of part thereof or a CHD-mimotope protein, fragment thereof or a CHD-mimotope polypeptide derived or derivable from an avian CHD gene.
20. A protein or fragment thereof, according to claim 19, which contains a CHD-chromobox and is derived or derivable from the nucleic acid sequence shown in Figure 5, Figure 7 or Figure 8.
21. A protein or fragment thereof or polypeptide containing a CHD-chromobox which is derived or derivable from the nucleic acid sequence shown in Figure 5, Figure 7 or Figure 8, including at least one of the characteristic amino acid residues at position 11, 12, 20, 27 or 31 inside the chromobox or 3, 6, 8, 12-15 or 16 directly downstream of the chromobox when aligned to best effect and as set out in Fig. 11.
22. A CHD-protein or fragment thereof or a polypeptide encoded by a nucleic acid or fragment or oligonucleotide according to claims 1-14 which is derived or derivable from the nucleic acid sequence shown in Figure 5, Figure 7 or Figure 8 and contains a CHD-chromobox
23. A process for controlling the sex of the progeny of a non-ratite bird comprising supplying exogenously to a cell of the bird or a progenitor of the bird a protein or fragment thereof or a polypeptide according to any one of claims 19-22
24. A process according to claim 23 wherein the protein or fragment thereof or polypeptide is supplied and activates a *CHD-1A* or *CHD-W* target gene.

AMENDED SHEET

25. An antibody or fragment thereof against a protein or fragment thereof or polypeptide according to any one of claims 19-22.
26. An antibody producing cell capable of expressing an antibody or fragment thereof according to claim 25.
27. Use of a protein or fragment thereof or polypeptide according to any one of claims 19-22 or antibody or fragment thereof or cell according to claims 25 or 26 in ascertaining the sex of an embryo cell or tissue of a non-ratite bird.
28. A transgenic or chimeric non-ratite bird having a heterologous nucleic acid or fragment or oligonucleotide according to any one of claims 1 to 14 in the genome of at least the germ cells of the bird.
29. Gametes of a non-ratite bird according to claim 28.
30. Progeny of a non-ratite bird according to claim 28.
31. Progeny according to claim 30 which are transgenic or chimeric and have a heterologous nucleic acid or fragment according to any one of claims 1-14 in the genome of at least the germ cells of the progeny.
32. A method of controlling the population of a species of bird which comprises introducing an individual member of the species into the population, said individual having a copy or copies of a nucleic acid fragment or oligonucleotide according to any one of claims 1 to 14 integrated on a chromosome (carrier chromosome) be it sex linked or autosomal whereby when the male breeds with other individuals of the population the progeny are substantially of one sex or are sexually dysfunctional intersexes.
33. A method according to claim 32 where the nucleic acid integrated into the carrier chromosome is homologous to the native *CHD-1A* or *CHD-W* gene of the bird.

AMENDED

1 Applicant or Patentee: RICHARD GRIFFITHS & BELA TIWARI Attorney's  
 2 Serial or Patent No.: \_\_\_\_\_ Docket No.: \_\_\_\_\_  
 3 Filed or Issued: \_\_\_\_\_  
 4 For: AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN BIRDS

VERIFIED STATEMENT (DECLARATION) CLAIMING SMALL ENTITY STATUS  
 (37 CFR 1.9(f) and 1.27(c)) - SMALL BUSINESS CONCERN

I hereby declare that I am

- 5 ☐ the owner of the small business concern identified below:  
 6 ☒ an official of the small business concern empowered to act on behalf of the concern identified below:

7 NAME OF CONCERN ISIS INNOVATION LIMITED  
 ADDRESS OF CONCERN 2 South Parks Road, Oxford, OX1 3UB, United Kingdom.

I hereby declare that the above identified small business concern qualifies as a small business concern as defined in 13 CFR 121.3-18, and reproduced in 37 CFR 1.9(d), for purposes of paying reduced fees under section 41(a) and (b) of Title 35, United States Code, in that the number of employees of the concern, including those of its affiliates, does not exceed 500 persons. For purposes of this statement, (1) the number of employees of the business concern is the average over the previous fiscal year of the concern of the persons employed on a full-time, part-time or temporary basis during each of the pay periods of the fiscal year, and (2) concerns are affiliates of each other when either, directly or indirectly, one concern controls or has the power to control the other, or a third party or parties controls or has the power to control both.

I hereby declare that rights under contract or law have been conveyed to and remain with the small business concern identified above with regard to the invention, entitled  
 4 AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN BIRDS by inventor(s)  
 1 RICHARD GRIFFITHS & BELA TIWARI  
 described in

- ☐ the specification filed herewith  
 2,3 ☐ application serial no. \_\_\_\_\_, filed \_\_\_\_\_  
 2,3 ☐ patent no. \_\_\_\_\_, issued \_\_\_\_\_

If the rights held by the above identified small business concern are not exclusive, each individual, concern or organization having rights to the invention is listed below\* and no rights to the invention are held by any person, other than the inventor, who could not qualify as a small business concern under 37 CFR 1.9(d) or by any concern which would not qualify as a small business concern under 37 CFR 1.9(d) or a nonprofit organization under 37 CFR 1.9(e). \*NOTE: Separate verified statements are required from each named person, concern or organization having rights to the invention averring to their status as small entities. (37 CFR 1.27)

8 NAME \_\_\_\_\_  
 9 ADDRESS \_\_\_\_\_  
 10 ☐ INDIVIDUAL ☐ SMALL BUSINESS CONCERN ☐ NONPROFIT ORGANIZATION  
 11 NAME \_\_\_\_\_  
 12 ADDRESS \_\_\_\_\_  
 13 ☐ INDIVIDUAL ☐ SMALL BUSINESS CONCERN ☐ NONPROFIT ORGANIZATION

I acknowledge the duty to file, in this application or patent, notification of any change in status resulting in loss of entitlement to small entity status prior to paying, or at the time of paying, the earliest of the issue fee or any maintenance fee due after the date on which status as a small entity is no longer appropriate. (37 CFR 1.28(b))

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application, any patent issuing thereon, or any patent to which this verified statement is directed.

NAME OF PERSON SIGNING TIM COOK  
 TITLE OF PERSON OTHER THAN OWNER Managing Director  
 ADDRESS OF PERSON SIGNING 2 South Parks Road, Oxford, OX1 3UB, United Kingdom.  
 SIGNATURE T Cook DATE 13/1/98

Figure 1.

CCCGGTCGGAGGTTTCAAGGAATGACTAGATGTGGCACTTAGTGCCATGGTCTAGTTGAC	60
AAGGTGATGGTTGGTCAAAAGTTGGACTCGATGATCTCAGAGTTTTTTTCCAGCCTTAAT	120
AATTCTATGAATTCGTAAATTTTATTCTTGATCTTTTTGAGCGAAGTTTGTGGGGATT	180
TTAGTTTGGTTTCCCTGTCAGTGTCTTCTTCTTGAAACTGACTTTCATTTGCAACATG	240
AGAATTGCTGTATTTGTCAGGTTACAAGTAGTGCAATGGCTGCTTAGAAGTAGTGAGAAA	300
CATTTAGGGAAATACTGGAGTGAAGCAAACACAGTGGTACTGCCAAACTGTAGCTTTGGG	360
ATTTGAGGAGCCACAGAGTTGTATATAAATTTGTTTAATGATATCCTGCCCCCTGCCTTCC	420
ATTAATTGCTTGTTTTATGAAACCACTCTTTTTTTTTTTTTTTTTTTTTTTGGCTTCTTCA	480
TATCCTGTGGTAATGAGTTAATGCATTTAGAAGCACATGGCAGAACTAGGAGATCTGTGG	540
ATGACAGTGGTACAGGAGCTCTGAATTTTTTAGATAAACTATGAGAGTGGAAACAGAAAT	600
CTGAGGCTAGTTTCTTGAGCTGACTGTAAATTTTGTGAGAATATTTTCAAGACTACATTA	660
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GGG	723



2/18

Figure 2.

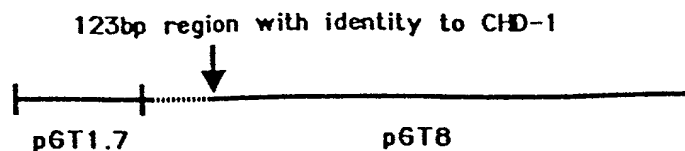


Figure 3.

M	CHD-1	ATTCTTCCAG	ATGATCCTGA	TAAAAACCA	CAAGCAAAC	AGTTACAGAC
C	CHD-1A	ATTTTACCTG	ATGATCCAGA	CAAGAAACCC	CAGGCAAAGC	AGCTACAGAC
C	CHD-W	ATTTTACCTG	ATGATCCAGA	TAAGAAACCC	CAGGCTAAGC	AGTTACAGAC
GT	CHD-W	ATTTTACCTG	ATGACCCAGA	TAAGAAACCA	CAGGCAAAGC	AGTTGCAGAC
M	CHD-1	CAAAAAACCA	CAAGCAAAC	AGTTACAGAC	CCGTGCAGAC	TACCTCATCA
C	CHD-1A	CAAGAAACCC	CAGGCAAAGC	AGCTACAGAC	CCGTGCAGAC	TACCTCATTA
C	CHD-W	CAAGAAACCC	CAGGCTAAGC	AGTTACAGAC	CCGTGCAGAT	TACCTCATTA
GT	CHD-W	CAAGAAACCA	CAGGCAAAGC	AGTTGCAGAC	CCGTGCAGAT	TACCTCATTA
M	CHD-1	AACTACTTAG	CAGAGATCTT	GCAAAAAGAG	AGGCTCAGAG	ACTTTGTGGT GCG
C	CHD-1A	AATTACTGAA	TAAAGACCTT	GCAAGAAAGG	AAGCACAAAG	GCTTGCTGGT GCA
C	CHD-W	AATTACTGAA	TAAAGACCTT	GCAAGAAAGG	AAGCACAGAG	ACTTGCTGGT GCA
GT	CHD-W	AATTACTGAA	TAAAGACCTT	GCAAGAAAAG	AAGTGCAAAG	ACTTACTGGT GCA

M	CHD-1	ILPDDPDKKPQAKQLQTRADYLIKLLSRDLAKREAQRLCGA
C	CHD-1A	ILPDDPDKKPQAKQLQTRADYLIKLLNKDLARKEAQRLAGA
C	CHD-W	ILPDDPDKKPQAKQLQTRADYLIKLLNKDLARKEAQRLAGA
GT	CHD-W	ILPDDPDKKPQAKQLQTRADYLIKLLNKDLARKEVQRLTGA
		*****

Figure 4.

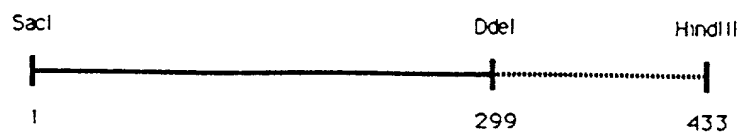


Figure 5.

1 CGGGCTGCGG CACGAAGCGC ACCGCCGGCG CACGCAGGCT CGGGCCGGGG  
 51 AAGGCTTGGC CCGCCGAGCC GGACGCACGC AGGTATTTGG GCAAAAATCT  
 101 TGGCCATCTG TAGAGAATAG CAAGTCAAAC GCATTACTTC GAAAACATAC  
 151 GGAGTACCAG AAAGGGGATT CTTGACCTAC ACCTTGTAAC CTGAGTGGAC  
 201 TTTCTTTTAA ACTTCTTAAT ACTTACAATG AATGGGCACA GTGATGAAGA  
 251 AAGTGTAAGA AACAGCAGTG GAGAGTCAAG CAGATCAGAT GATGATTCTG  
 301 GGTCAAGTTC AGGTCTGGA TCTGGTTCAA GCTCTGGAAG CAGTAGCGAT  
 351 GGAAGTAGCA GCCAGTCAGG TAGCAGTGAC TCTGAATCTG GTTCAGAGTC  
 401 AGGCAGTCAA TCCGAATCAG AGTCTGACAC ATCTAGAGAG AAGAAACAAG  
 451 TTCAAGCTAA ACCTCCGAAA GCTGACGGAT CTGAGTTTTG GAAGTCCAGT  
 501 CCAAGCATAC TTGCTGTACA GAGATCAGCA GTGCTCAAGA AGCAACAGCA  
 551 ACAGCAAAAA GCAGCATCAT CAGACAGTGG TTCAGAAGAG GACTCATCCA  
 601 GTAGTGAAGA TTCTGCCGAT GATTTCGTCCA GTGAAACTAA GAAGAAAAAG  
 651 CATAAAGATG AAGACTGGCA AATGTCAGGG TCAGGGTCAG TATCAGGAAC  
 701 TGGTTCTGAT TCTGAATCGG CGGAAGATGG GGATAAAAGC AGTTGTGAAG  
 751 AAAGTGAATC TGAATATGAG CCAAAAAACA AAGTCAAAAG CCGTAAACCT  
 801 CCAAGCAGAA TTAAGCCAAA AAGTGGGAAA AAGAGCACAG GACAGAAGAA  
 851 GAGGCAACTT GATTTCATCAG AGGAGGAGGA GGACGATGAT AAAGATTATG  
 901 ATAAGAGAGG ATCTCGTCGC CAGGCAACAG TGAATGTTAG TTACAAAGAA  
 951 GCTGAAGAAA CCAAGCAGAA TTCTGATGAT TTGCTGGAAG TTTGTGGAGA  
 1001 GGATGTCCCA CAGACTGAAG AAGATGAATT TGAAACTATA GAGAAGTTTA  
 1051 TGGACAGTCG AATTGGCCGA AAAGGAGCCA CTGGTGCCTC AACCACCATC  
 1101 TATGCCGTTG AGGCAGATGG TGACCCAAAT GCTGGGTTTG AAAAGTCAAA  
 1151 GGAGCTGGGA GAAATACAGT ATCTTATTAA ATGGAAAGGC TGGTCACACA  
 1201 TCCATAACAC TTGGGAAACT GAAGAAACGC TGAAGCAACA AAATGTTAAA  
 1251 GGAATGAACA AACTGGACAA CTACAAGAAA AAGGATCAGG AGACAAAACG  
 1301 CTGGCTGAAA AATGCTTCTC CAGAAGATGT CAGAAATATT AACTGCCAGC  
 1351 AGGAGCTTAC AGATGATCTG CACAAACAAT ATCAAATAGT GGAAGAATA  
 1401 ATTGCTCATT CAAATCAAAA GTCAGCAGCT GGTATCCGG ACTACTATTG  
 1451 CAAATGGCAG GGTCTGCCTT ACTCAGAATG TAGCTGGGAA GATGGTGCCTC  
 1501 TCATTGCCAA AAAGTTTCAG GCACGCATTG ATGAGTATTT TAGCAGAAAT  
 1551 CAATCCAAGA CTACTCCCTT TAAGGACTGC AAGGTTCTAA AACAGAGACC  
 1601 AAGATTTGTT GCACGTAAGA AGCAACCATC TTACATTGGA GGACATGAAA  
 1651 GTCTGGAGTT AAGAGATTAT CAGTTAAATG GATTGAATTG GCTCGCTCAT  
 1701 TCATGGTGCA AAGGAAATAG TTGTATTCTT GCAGATGAAA TGGGTCTGGG  
 1751 TAAACAATA CAAACAATTT CTTTCTGAA CTACCTGTTT CATGAACATC  
 1801 AACTGTATGG CCCTTTTCTT CTGCGCTGTC CACTTTCTAC CTTGACATCT  
 1851 TGGCAAAGAG AGATTCAAAC TTGGGCTCCT CAGATGAATG CTGTAGTTTA  
 1901 CTTAGGAGAT ATAACATGTA GAAATATGAT AAGGACTCAT GAATGGATGC  
 1951 ATCCACAGAC TAAACGATTA AAGTTTAAAC TACTTCTGAC GACATATGAA  
 2001 ATTTTACTGA AGGATAAGTC ATTCCTTGGT GGTCTCAATT GGGCATTCTAT  
 2051 AGGAGTTGAT GAAGCTCATC GTTTAAAAAA TGATGACTCT CTTCTGTACA  
 2101 GGACTTTAAT AGACTTTAAG TCCAACCATC GACTTCTGAT TACTGGAACC  
 2151 CCACTGCAAA ATTCCCTCAA AGAGCTGTGG TCTTTGTTGC ATTTTCATCAT  
 2201 GCCAGAAAAA TTTTCCTCCT GGGAAAGATT TGAAGAGGAG CATGGCAAAG  
 2251 GAAGAGAGTA TGGTTATGCA AGTCTTCACA AAGAGCTTG ACCATTTTAA  
 2301 CTAAGAAGAG TTAAGAAAGA TGTAGAAAAG TCTTTACCTG CTAAGGTTGA  
 2351 ACAAATTCAG AGGATGGAAA TGAGTGCAAT GCAGAAGCAA TATTACAAGT  
 2401 GGATTTTAAC AAGGAATTAT AAAGCCCTCA GTAAAGGTTT AAAAGGCAGT  
 2451 ACCTCAGGCT TTCTGAACAT TATGATGGAA CTTAAGAAAG GTTGTAAACA  
 2501 TTGCTACCTC ATTAAGCCAC CAGATGATAA TGAATCTAT AATAAACAGG  
 2551 AGGCCTTACA GCATTTGATA CGTAGCAGCG GGAAGCTAAT CTTCTTGAC  
 2601 AAGCTACTGA TTCGTCTGCG AGAACGTGGC AACAGAGTTC TGATTTTCTC  
 2651 TCAGATGGTG AGGATGCTGG ACATCCTAGC AGAATATCTG AAGTATCGCC  
 2701 AGTTTCCCTT CCAGAGACTT GATGGATCAA TAAAAGGGGA ATTGAGGAAG  
 2751 CAAGCACTGG ATCATTTCAC TGCAGAAGGA TCAGAGGATT TCTGTTTTTT  
 2801 ACTGTCTACA AGAGCTGGAG GATTAGGTAT TAAGTTGGCA TCTGTGTACA  
 2851 CTGTAGTTAT TTTTGATTCT GACTGGAATC CACAGAATGA TCTGCAGGCA  
 2901 CAGGCGAGAG CTCATAGAAT TGGACAGAAG AAACAGGTTA ATATTTATCG  
 2951 GCTAGTCACA AAAGGATCAG TAGAAGAAGA TATTCTTGAA AGAGCCAAGA

3001 AGAAGATGGT GCTAGACCAT TTAGTAATTC AGAGAATGGA CACGACAGGA  
 3051 AAAACTGTTC TGCATACAGG TTCAACTCCA TCAAGCTCTA CACCTTTTAA  
 3101 TAAAGAAGAG TTATCAGCTA TTTTGAAAGT TGGTGCTGAG GAACTCTTTA  
 3151 AAGAACCCTGA AGGAGAAGAA CAGGAGCCCC AGGAAATGGA TATAGATGAA  
 3201 ATCTTGAAGA GAGCTGAAAC TCGGGAAAAT GAGCCAGGTC CATTGACTGT  
 3251 AGGGGATGAG TTGCTTTCAC AGTTCAGGT GCGGAACCTT TCCAATATGG  
 3301 ATGAAGATGA TATTGAGTTG GAACCAGAAA GAAATTCAG AAATTGGGAA  
 3351 GAAATCATCC CAGAAATCCA ACGGAGAAGG ATAGAGGAGG AGGAAAGACA  
 3401 AAAAGAACTT GAAGAAATAT ACATGCTCCC GAGGATGAGA AACTGTGCAA  
 3451 AACAGATCAG CTTTAATGGG AGTGAAGGAA GACGCAGTAG GAGCAGAAGA  
 3501 TATTCTGGAT CTGATAGTGA CTCCATCACA GAAAGAAAAC GGCCAAAAAA  
 3551 GCGTGGAAGA CCTCGAACCA TTCCTCGAGA AAATATTAAA GGATTTAGTG  
 3601 ATGCAGAGAT CAGGCGGTTT ATCAAGAGTT ACAAGAAAT TGGTGGCCCT  
 3651 CTGGAAAGGT TAGATGCTGT AGCTAGAGAT GCTGAACTGG TTGATAAATC  
 3701 TGAGACAGAC CTTAGACGTT TGGGTGAAC TGTACATAAT GGATGCATTA  
 3751 AGGCTTTAAA GGACAATTCA TCTGGACAAG AAAGAGCAGG AGGTAGACTT  
 3801 GGGAAAGTTA AAGGCCCAAC GTTTCGAATC TCAGGAGTGC AGGTGAATGC  
 3851 AAAACTAGTC ATCTCTCAG AAGAAGAGCT GGCACCACTG CACAAATCCA  
 3901 TTCCTTCAGA TCCAGAAGAA AGGAAAAGAT ATGTCATCCC ATGCCACACC  
 3951 AAGGCTGCTC ACTTCGATAT AGATTGGGGT AAAGAAGATG ATTCCAATCT  
 4001 GTTAGTAGGC ATCTATGAAT ATGGCTATGG CAGCTGGGAA ATGATAAAAA  
 4051 TGGATCCAGA TCTCAGCTTA ACACAGAAGA TTTTACCTGA TGATCCAGAC  
 4101 AAGAAACCCC AGGCAAAGCA GCTACAGACC CGTGCAGACT ACCTCATTAA  
 4151 ATTACTGAAT AAAGACCTTG CAAGAAAGGA AGCACAAAGG CTTGCTGGTG  
 4201 CAGGCAATTC CAAGAGAAGG AAGACAAGAA ATAAGAAGAA TAAGATGAAG  
 4251 GCTTCAAAAA TAAAAGAAGA AATAAAGAGT GATTCTTCAC CACAACCTC  
 4301 AGAAAAATCT GATGAAGATG ATGAGGAGGA GGATAACAAG GTAAATGAAA  
 \*\*  
 4351 TGAAATCTGA AAATAAAGAA AAATCTAAAA AAATTCATT GCTGGATACT  
 4401 CCAGTTCATA TTACTGCAAC CAGTGAACCA GTTCTATCT CAGAAGATCT  
 4451 TGAAGAAGCT CATCAGAAGA CATTAGTGT GTGCAAAGAA AGAATGAGGC  
 4501 CTGTCAAAGC AGCACTGAAA CAGCTGGATA GACCAGAGAA GGGCCTTTCT  
 4551 GAAAGGGAGC AGCTGGAACA TACTAGGCAG TGTCTAATCA AAATTGGGGA  
 4601 TCACATTACA GAATGCCTGA AGGAGTACAC AAATCCCGAG CAAATAAAAC  
 4651 AGTGGAGGAA AAATTTGTGG ATTTTGTGT CCAAGTTTAC AGAATTTGAT  
 4701 GCCAGAAAGC TGCACAAACT CTACAAACAT GCAATCAAAA AGCGCCAAGA  
 4751 GCTCTAGCAA CACAATGACC AAAACATTAG CAGCAATGTG AATACACATG  
 4801 TAATCAGAAA TCCAGATGTG GAAAGACTGA AGGAGACTAC AAACCATGAT  
 4851 GATAGTAGCA GGGACAGTTA TTCTTCTGAT AGACATTTAT CACAATACCA  
 4901 TGATCATCAC AAAGACAGGC ATCAGGGAGA TGCTTACAAG AAAAGTGACT  
 4951 CCAGGAAAAG GCCATATTCA GCCTTCAGTA ATGGAAAAGA TCACAGAGAC  
 5001 TGGGATCACT ACAAACAGGA CAGCAGATAC TACAGTGATA TCAATACATAG  
 5051 AAAGTTAGAT GACCACAGGA GCAGAGACCA CAGGTCAAAC CTGGAAGGAA  
 5101 ACTTAAAAGA CAGCCGGGGT CATTGAGATC ACCGCTCCCA TTCAGACCAC  
 5151 AGGATACACT CAGATCACCG TTCCACTTCA GAATACAGCC ATCATAAATC  
 5201 TTCGAGAGAT TATAGATACC ACTCAGACTG GCAAATGGAC CACAGAGCTT  
 5251 CTGGTAGTGG CCCGAGGTCA CCACTAGATC AGAGGTCTCC TTTATGGTTCA  
 5301 AGATCTCCCC TAGGACACAG ATCTCCATTT GAACACTCAT CAGATCACAA  
 5351 AAGTACACCT GAACATACAT GGAGTAGCCG GAAGACATAA CAAAGACTGA  
 5401 CATTTTCTGG ACCTTCTTTT TAGCCATATA CAGTAAACTA ACACAGTAAT  
 5451 TGCCTTACAT GACTTGAAAG ATATGGACTG GATATTCTAT CAGTAGCAGT  
 5501 ATTGTTACTT CTTTCCAGGA TGCAAGGTCT ATTATCCCAA CAGAAGAAAA  
 5551 ATATTTTGTG ATTTAAAGTT TATGCTGCAC TGTGCTGCAA ATGTTGTGGC  
 5601 ACTTTTTTTT TAAGAAATGG AAGATGTTTA CTTTTACAGG GACCTCAACA  
 5651 CTGCCCCCTT CAGACTGGAT CTTACTATAA AACTCTTCAT GTCAAAGTGG  
 5701 TTCTAGGCTG AACACAGATT AAATTATGTT TGTAAATGAA CACTTAAACA  
 5751 CTGACCTGTG CTTATGTTT AGGAAAGAAT GGGGATTTA TTTTGTTTTA  
 5801 TTTCTTGGTA GAGAACTCTC AAGGACTTTG TTCACTTTCC AAAGCTACTT  
 5851 GTTACATTG TACACTGCGA CCACCTTGCC GCTTTTCATC ACAAGCTTGA  
 5901 ATATTTAAAT TCTGTACCTA CAGTTGTAAA ATAGCCAGGA TTTCTCCTGT  
 5951 TTGTGATCAG TTATAATGCC TTTTATGAA ACAAACAAAC AAACAAAAAA  
 6001 CAATTAATAA AAAAAACACA ACAAACCAA CAAATGGCTG TAAATATTATG  
 6051 TAAATTAATT AAATGAGCTT TTTTCCGTCA GGCTTTTTTT GGCTGTTCCCT  
 6101 TTCCCCAACA ACTCAGGCCT TCTTTTCACA AAGTCAGTAT ACTTACATGT  
 6151 TTTAATAAAA TATCTCGATG GAATCAGAAT GTAAAAATGG GGAAGGGAAT  
 6201 ATTTTATTC ATTTAGTGCT CCTTTTAT TGGATACTTT TACATACCTG  
 6251 TTTTGGTTG TTTTATTTA TTTTTTTTT CTATTAACT GTCAGTGTG  
 6301 TGATTGTTG AATGAACAGT GAGAATATCC CACTCTAAAC TGTGCCCTGG  
 6351 AAAGCTTTTC AGGTGCATTG GTTAAAAGA AGGAAGTGTT CTATAGGTGA

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6401 ACACTTCAAA ACCCAGATCA GCCAAGATTC ATTGTAAATC CATTGTGTTT  
6451 CCCTCTTTAA CATGGGCAAT AATGTCAAAT GTGCTATGCA GCAGTTAATA  
6501 TTTTAGAAGA TTTGAATGAC TTTATTAACA GAATTGTTAC AATGCACACT  
6551 GATTGTACAT AGATAACTTC TATCTGACAA ATTAAATTAA CTAAAACCAA  
6601 AAAAAACC

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Figure 6.

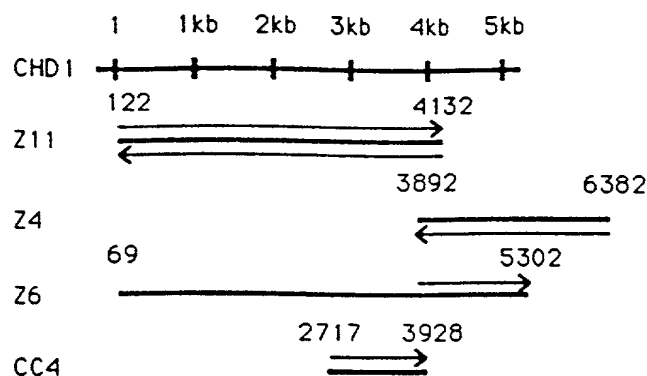


Figure 7.

		D E I V S V K H L H K K I K T E
CHD-1A	1	GATGAGATTGTTTCAGTGAAACATCTACATAAAAAAATAAAACAGAAA
CHD-W	1	GATGGGATTGTTTCAGTGAAACATCCACATAAAAAAATAAAAGCAGAAA
		D G I V S V K H P H K K I K A E
		K E N E E K P E P D I G I K K E A
CHD-1A	51	AAAGAAAATGAAGAAAAGCCTGAGCCAGATATTGGTATAAAGAAGGAAGCT
CHD-W	51	AAAGAAAATGAAGAAAAGATGAGCCAGAGATTGGTATAAAGAAGGAAGCT
		K E N E E K D E P E I G I K K E A
		E E K R E T K E K E N K R E L K R
CHD-1A	101	GAAGAAAAAGAGAGACAAAAGAGAAGGAAAATAAAAGGGAATTGAAAAGG
CHD-W	101	GGAGAAAAAGAGAGACAAAAGAAAAGGAAAATAAGA
		G E K R E T K E K E N K
		E K K E K E D K K E L K E K D N K
CHD-1A	151	GAGAAAAAGAAAAGAGGATAAGAAAGAATTAAAGAAAAGATAATAAA
		E K R E N K V K E S T Q K E K E V
CHD-1A	201	GAAAAGAGAGAAAACAAAGTAAAGAATCCACACAGAAAAGAAAAGAAAGTG
		K E E K
CHD-1A	251	AAGGAAGAGAAG

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Figure 8.

ATTTATCGGC	TAGTCACAAA	AGGATCAGTA	GAAGAAGATA	TTCTTGAAAG	AGCCAAGAAA	AAGATGGTGT	TAGATCATTT
10	20	30	40	50	60	70	80
AGTGATTCAG	AGAATGGACA	CCACAGGGAA	AACTGTACTA	CATACAGGCT	CTACTCCTTC	AAGCTCAACA	CCTTTTAATA
90	100	110	120	130	140	150	160
AGGAAGAGTT	ATCAGCAATT	TTGAAGTTTG	GTGCTGAGGA	ACTTTTAAAA	GAACCTGAAN	NNGAAGAAGA	GGAGCCTCAG
170	180	190	200	210	220	230	240
GAGATGGATA	TAGATGAAAT	CCTGAAGAGG	NCTGAAATC	GAGAAAATGA	GTCAGGCCCA	TTAACTGTAG	GAGATGAGTT
250	260	270	280	290	300	310	320
ACTTTCACAG	TTCAAGGTAG	CTAACTTTTC	CAATATGGAT	GAAGATGACA	TTGAATTGGA	ACCAGAACAA	AATCTAAGAA
330	340	350	360	370	380	390	400
ACTGGGAAGA	AATCATTCCA	GAAGTTCAGT	GGCGACGAAT	AGAGGGGNG	GAAAGACAAA	AAGAACTTGA	AGAAATATAT
410	420	430	440	450	460	470	480
ATGCTTCCAA	GAATGAGAAA	CTGTGCAAAA	CAGATCAGCT	TTAATGGAAA	TGAAGGGAGA	TGCAGTAGGA	GCAGAAGATA
490	500	510	520	530	540	550	560
TTCTGGATCT	GATAGTGATT	CCATCTCAGA	AAGAAAACGA	CCAAAAAAC	GTGGACGACC	ACGAATATT	CCCCGTGAAA
570	580	590	600	610	620	630	640
ACATTAAAGG	ATTTAGTGAT	GCAGAGATTA	GACGATTTAT	CAAGAGTTAC	AAGAAATTG	GTGCCCCAGT	TGAAAGGTTA
650	660	670	680	690	700	710	720
GATGCTATAG	CTAGAGATGC	TGAGCTAGTT	GATAAATCTG	AAACAGACCT	TAGACGCTG	GGAGAATTG	TACATAATGG
730	740	750	760	770	780	790	800
ATGCATTAAG	GCTTTAAATG	ATAATGACTT	TGGTCAAGGA	AGAACAGGTG	GTAGATTTGG	GAAAGTTAAA	GGOCCAACAT
810	820	830	840	850	860	870	880
TCCGAATAGC	AGGAGTGCAG	GTGAATGCAA	AGCTAGTCAT	TTCTCACGAA	GAAGAGTTGG	CACCATTGCA	TAAATCGATT
890	900	910	920	930	940	950	960
CCTTCAGATC	CAGAAGAAAG	GAAAAGATAT	GTGATCCCAT	ACCACACCAA	AGCAGCTCAT	TTTGATATAG	ATTGGGGTAA
970	980	990	1000	1010	1020	1030	1040
AGAAGATGAT	TCCAATCTGT	TAATAGGCAT	CTATGAATAT	GGTTATGGCA	GTTGGGAAAT	GATAAAAAATG	GATCCTGATC
1050	1060	1070	1080	1090	1100	1110	1120
TCAGTTTGAC	ACAGAAGATT	TTACCTGATG	ATCCAGATAA	GAAACCCAG	GCTAAGCAGT	TACAGACTOG	TGCAGATTAC
1130	1140	1150	1160	1170	1180	1190	1200
CTCATTAAAT	TACTGAATAA	AGACCTTGCA	AGAAAGGAAG	CACAGAGACT	TGCTGGTGCA	GGCAATTCAA	AGAGGAGAAA
1210	1220	1230	1240	1250	1260	1270	1280
AACAAGAAGT	AAGAAGAATA	AAGCAACAAA	GGCTGC				
1290	1300	1310					

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Figure 9.

§

C CHD-1A DARRYLGNLGH\*RIASQTHYFENIRSTRKGILDHLVT\*VDFLNFILITMNGHSDEE  
M CHD-1 FALCPFVTOREPQETRECRKFIIFEILIFEICITHILLIGDFCFINFLIFTMNGHSDEE  
\*\*\*\*\*

C CHD-1A SVRNSSGESSRSDDDSGSASGSGSGSSSGSSSDGSSSQSGSSDSESGSESGSQSESED  
M CHD-1 SVRNSSGESSQSGDD-CGSASGSGSGSSSGSSSDGSSSQSGSSDSDSGSDSGSQSESED  
\*\*\*\*\*

C CHD-1A TSREKKQVQAKPPKADGSEFWKSSPSILAVORS AVLKKQOOQ---QKAASSDSGSEEDSS  
M CHD-1 TSRENK-VQAKPPKVDGAZFWKSSPSILAVORSAMLKQPOQAQQRPASSNSGSEEDSS  
\*\*\*\*\*

C CHD-1A SSEDSDADDSSSETKKKKHKDEDWQMSGSGSVSGTGSDESSEZDGDKSSCEESESDYEPKN  
M CHD-1 SSEDSD-DDSSSGAKKKHNDWQMSGSGSPQLGSDSESEERDKSSCDGTESDYEPKN  
\*\*\*\*\*

C CHD-1A KVKSRKPPSRIKPKSGKKSTQKKRQLDSSEEEEDDEDYDKRGSRRQATVNVSYKEAEZ  
M CHD-1 KVRSRKPPNRKSKNGKKILGQKQRQIDSEDEDEDDYDNDKRSRRQATVNVSYKEDEE  
\*\*\*\*\*

C CHD-1A TKTDSDDLLEVCGEDVFPQTEDEFETIEKFMDSRIGRKATGASTTIYAVEADGDPNAGF  
M CHD-1 MKTDSDDLLEVCGEDVFPQPEDEEFETIERVMDCRVGRKATGATTIYAVEADGDPNAGF  
\*\*\*\*\*

C CHD-1A KTXEICEIQYLIKWKGWSHIHTWEETETLKQONVRCMKLDNYKKQDQETKRWLNAS  
M CHD-1 EKSKEICEIQYLIKWKGWSHIHTWEETETLKQONVRCMKLDNYKKQDQETKRWLNAS  
ERNKEICEIQYLIKWKGWSHIHTWEETETLKQONVRCMKLDNYKKQDQETKRWLNAS  
\*\*\*\*\*

HUMAN PEDVEYYNCQQLTDDLEKQYQIVERTNAXSPQSKSAAGYP  
C CHD-1A PEDVEYYNCQQLTDDLEKQYQIVERI IABSNQKSAAGYPDYCKWQGLPYSECSWEDGA  
M CHD-1 PEDVEYYNCQQLTDDLEKQYQIVERI IABSNQKSAAGLPDYCKWQGLPYSECSWEDGA  
\*\*\*\*\*

C CHD-1A LIAKKFQARIDEYFSRNQSKTTPFKDCKVLKQRPFRVALKKQPSYIGGHEE SLELRDYQLN  
M CHD-1 LISKFTQTCIDEYFSRNQSKTTPFKDCKVLKQRPFRVALKKQPSYIGGHEE SLELRDYQLN  
\*\*\*\*\*

C CHD-1A GLNWLABSWCKGNSCILADEMGLGKTIQTISFLNYLFHEBQLYGPFLLRVPLSTLTSWOR  
M CHD-1 GLNWLABSWCKGNSCILADEMGLGKTIQTISFLNYLFHEBQLYGPFLLRVPLSTLTSWOR  
\*\*\*\*\*

C CHD-1A EIQTWAPQMNNAVYVYLGDISRNMRITHEWHEPQTKRLKFNILLTTYE ILLKDKSFLGGLN  
M CHD-1 EIQTWASQMNNAVYVYLGDISRNMRITHEWHEPQTKRLKFNILLTTYE ILLKDKAFGLGGLN  
\*\*\*\*\*

C CHD-1A WAFIGVDEAHLKNDOSLLYRTLIDFKSNHRLITGTPLQNSLKEWLSLHFIPEKPFSS  
M CHD-1 WAFIGVDEAHLKNDOSLLYKTLIDFKSNHRLITGTPLQNSLKEWLSLHFIPEKPFSS  
\*\*\*\*\*

C CHD-1A WEDFEEZBGKGREYGYASLHKELEPFLLRVVKDVEKSLPAKVEQILRMESALQKQYYK  
M CHD-1 WEDFEEZBGKGREYGYASLHKELEPFLLRVVKDVEKSLPAKVEQILRMESALQKQYYK  
\*\*\*\*\*

C CHD-1A WILTRNYKALSKGSGSTSGFLNIMZLKKCCNHCYLIKPPDDNEFYNKQZALQHLIRSS  
M CHD-1 WILTRNYKALSKGSGSTSGFLNIMZLKKCCNHCYLIKPPDDNEFYNKQZALQHLIRSS  
\*\*\*\*\*

C CHD-1A GKLIILLDKLLIRLRERGNRVLI F SQMVRMLDILAEYLKYRQFPFQRLDGSIKGELRKQAL  
M CHD-1 GKLIILLDKLLIRLRERGNRVLI F SQMVRMLDILAEYLKYRQFPFQRLDGSIKGELRKQAL  
\*\*\*\*\*



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C CHD-1A  
M CHD-1

DHFNAEGSEDFCFLSTRAGGLGINLASADTVVIFDSOWNPQNDLQAAHRIQKKQV  
DHFNAEGSEDFCFLSTRAGGLGINLASADTVVIFDSOWNPQNDLQAAHRIQKKQV  
\*\*\*\*\*

C CHD-W  
C CHD-1A  
M CHD-1

-IYRLVTKGSVEEDILERAKKMMVLDHLVIQMDTTGKTVLHTGSTPSSSTPFNKEZLSA  
NIYRLVTKGSVEEDILERAKKMMVLDHLVIQMDTTGKTVLHTGSTPSSSTPFNKEZLSA  
NIYRLVTKGSVEEDILERAKKMMVLDHLVIQMDTTGKTVLHTGSTPSSSTPFNKEZLSA  
\*\*\*\*\*

C CHD-W  
C CHD-1A  
M CHD-1

ILKFGAEELFKPEPEKEEPEQEMDIDEILKRAETRENEPGPLTVGDELLSQFKVANFSNM  
ILKFGAEELFKPEPEKEEPEQEMDIDEILKRAETRENEPGPLTVGDELLSQFKVANFSNM  
ILKFGAEELFKPEPEKEEPEQEMDIDEILKRAETRENEPGPLTVGDELLSQFKVANFSNM  
\*\*\*\*\*

C CHD-W  
C CHD-1A  
M CHD-1

DEDDIELEPEQNLRNWEEIPEVQWRRIEGKERQKELEIYMLPRMRNCAQISFNGREG  
DEDDIELEPERNSKNWEEIPEEQRRRIEKEERQKELEIYMLPRMRNCAQISFNGSEG  
DEDDIELEPERNSRNWEEIPEEQRRRIEKEERQKELEIYMLPRMRNCAQISFNGSE  
\*\*\*\*\*

C CHD-W  
C CHD-1A  
M CHD-1

RCSRSRRYSGSDSDSISERKRPKRGPRPTIPRENIGFSDAEIRRFIKSYKFGGPFVR  
RRSRSRRYSGSDSDSISERKRPKRGPRPTIPRENIGFSDAEIRRFIKSYKFGGPFVR  
RRSRSRRYSGSDSDSISERKRPKRGPRPTIPRENIGFSDAEIRRFIKSYKFGGPFVR  
\*\*\*\*\*

C CHD-W  
C CHD-1A  
M CHD-1

LDAIARDAELVDKSETDLRRLGELVHNGCICALNDNDFQGRTRGRFGVKGPTFRISGV  
LDAIARDAELVDKSETDLRRLGELVHNGCVKALKDSSSGTERAGGRIGVKGPTFRISGV  
LDAIARDAELVDKSETDLRRLGELVHNGCICALNDNDFQGRTRGRFGVKGPTFRISGV  
\*\*\*\*\*

C CHD-W  
C CHD-1A  
M CHD-1

QVNAKLVISHEEELAPLHKSIPSDPEERKRYVIPYHTKAAHFDIDWGEKEDSNLLIGIYE  
QVNAKLVIHAEDELIPLEKSIPSDPEERKRYVIPYHTKAAHFDIDWGEKEDSNLLIGIYE  
QVNAKLVISHEEELAPLHKSIPSDPEERKRYVIPYHTKAAHFDIDWGEKEDSNLLIGIYE  
\*\*\*\*\*

C CHD-W  
C CHD-1A  
M CHD-1

YGYGSWEHMKMDPDLSTQKILPDDPKKQAKQLQTRADYLIKLLNKDLARKEAQRLAG  
YGYGSWEHMKMDPDLSTQKILPDDPKKQAKQLQTRADYLIKLLNKDLARKEAQRLAG  
YGYGSWEHMKMDPDLSTQKILPDDPKKQAKQLQTRADYLIKLLNKDLARKEAQRLAG  
\*\*\*\*\*

C CHD-W  
C CHD-1A  
M CHD-1

AGNSKRRKTRSKKATKAA  
AGGSKRRKTRAKSKAMKSIVKEEIKSDSSPLPSEKSEDEDD---KLNDSKPEKDRS  
AGNSKRRKTRSKKATKAA  
\*\*\*\*\*

C CHD-1A  
M CHD-1

KKSVVSDAPVHITASGEVPVIAEELDQKTFISICKERMRFVKAALKQLDRPEKGLSER  
KKIPLLOTVPVHITATSEKVPVIAEELDQKTFISICKERMRFVKAALKQLDRPEKGLSER  
\*\*\*\*\*

C CHD-1A  
M CHD-1

EQLEHTRQCLIKIGDHITECLKEYSNPEQIKQWRKLNWIIVSKPTEFDARKLEKLYKHA  
EQLEHTRQCLIKIGDHITECLKEYSNPEQIKQWRKLNWIIVSKPTEFDARKLEKLYKHA  
\*\*\*\*\*

C CHD-1A  
M CHD-1

KKROESQONSDQN-SNVATTHVIRNPDMERLKENTNHDSSRDSYSSDRHLSQYHDHEKD  
KKROESQONSDQN-SNVATTHVIRNPDMERLKENTNHDSSRDSYSSDRHLSQYHDHEKD  
\*\*\*\*\*

C CHD-1A  
M CHD-1

RHQGDSYKKSDSRKRPSYSSNGKDEREWDHYRQDSRYSDREKHKRLDDHRSREHRPSL  
RHQGDAYKKSDSRKRPSYSSNGKDEREWDHYRQDSRYSDREKHKRLDDHRSREHRPSL  
\*\*\*\*\*

C CHD-1A  
M CHD-1

EGGLKD-RCHSDHRSBSHDSHERSTPSTHIIINPRDYRYLSDWQLDERAASSGPRSP  
EGNLKDSRGHSBHSBHSHERSTPSTHIIINPRDYRYLSDWQLDERAASSGPRSP  
\*\*\*\*\*

C CHD-1A  
M CHD-1

LDQRSPYGSRSRSP-----FEHSAEHRSTPEHTWSSRKTQXQLMSLSSGTLFXP  
LDQRSPYGSRSRSPFEHSSDHKSTPEHTWSSRKTQXQLMSLSSGTLFXP  
\*\*\*\*\*

C CHD-1A  
C CHD-1A  
C CHD-1A  
C CHD-1A  
C CHD-1A  
C CHD-1A  
C CHD-1A

LTXLERYGLDILSVAVILLISRMQGLLSQKKNIFVKVYALCCKCCGTFILNRCILL  
LQGPQBCFPQTGSYYKTLBVVVLGXTQIKLCIXMNTXLTCAVYSGKNGGILFYFLVE  
NSQGLCSLSKATCLBCTLRPPCRFSSQAXIFKCTYSCKIARISPVCDQLXCLFMKQTNK  
QKTIKQNTTKPTNOCKLLXINXMSFFPSGFWLFLSPTTQAFISQSYTYTFXNISMK  
SECKNGEINILFHLVLLFYWILLBCTFWLFFYIFFFYXTVSVVIVVNSENIPLXTVFWK  
AFQVHWTKRRKCSIGZHFATQISQDSLXIHLSLFPNMGNVVKCAMQQLIFXKIXMTLLTE  
LLQCTLIVHXLSDKLNKXKPKKT

**SUBSTITUTE SHEET (RULE 26)**

[illegible]

**SUBSTITUTE SHEET (RULE 26)**

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Figure 11.

CCHD	AVEAD	GDPNAGFEKSKELGE.IQYLIKWKGWSHIHTWETEET	LKQQNVKGMNKL DNYKK
MCHD	AVEAD	GDPNAGFERNKEPGD.IQYLIKWKGWSHIHTWETEET	LKQQNVRGNKKL DNYKK
YCHD	EGKVL	EKTVPDLNNCKE..N.YEFLIKWTDESHLENTWETYES	IGQ..VRGLKRL DNYCK
		**          ****    **          *****	*    *    *    *****    *
DHP1	EEEE	YAVEKIIDRRVRK GK.VEYLLKWKGY PETENTWEPENN	LDCQDLIQQY
HHP1	EDEE	YVVEKVLDRRVVKGKQVEYLLKWKGFSEEHNTWEPEN	LDCPELISEF
MMOD1	EEEE	YVVEKVLDRRVVKGK.VEYLLKWKGFSDENTWEPEN	LDCPDLIAEF
MMOD2	AEPE	FVVEKVLDRRVVNGK.VEYFLKWKGFTDADNTWEPEN	LDCPELIEDF
	**	***    ****    **    ***    *****    *****	***    **
DPC	PVDLV	YAAEKIIQKRVKKG V.VEYRVKWKGW NQRYNTWEPENN	ILDRRLIDIY
MMOD3	VGEQV	FAAECILSKRLRK GK.LEYLVKWRGWSSKHSWEPEEN	ILDPRLLLAF
	*	***    *    **    ***    ***    *****    *    *****	*****
		^^                    ^    ^^	

Figure 12.

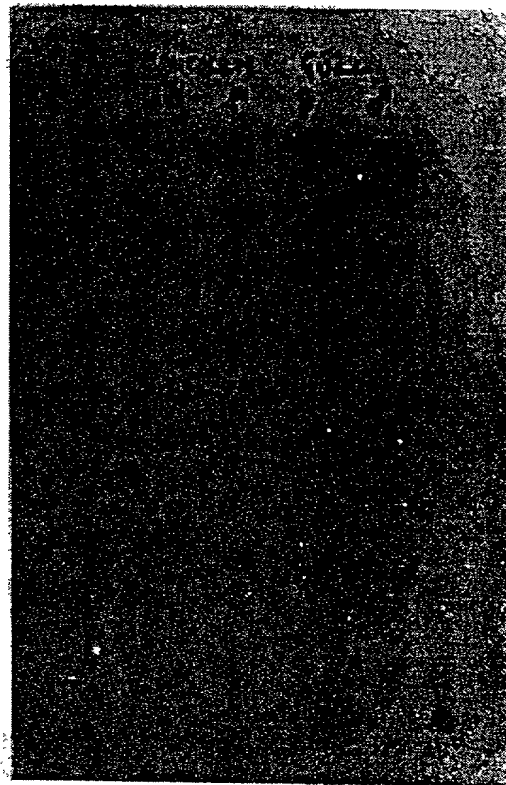
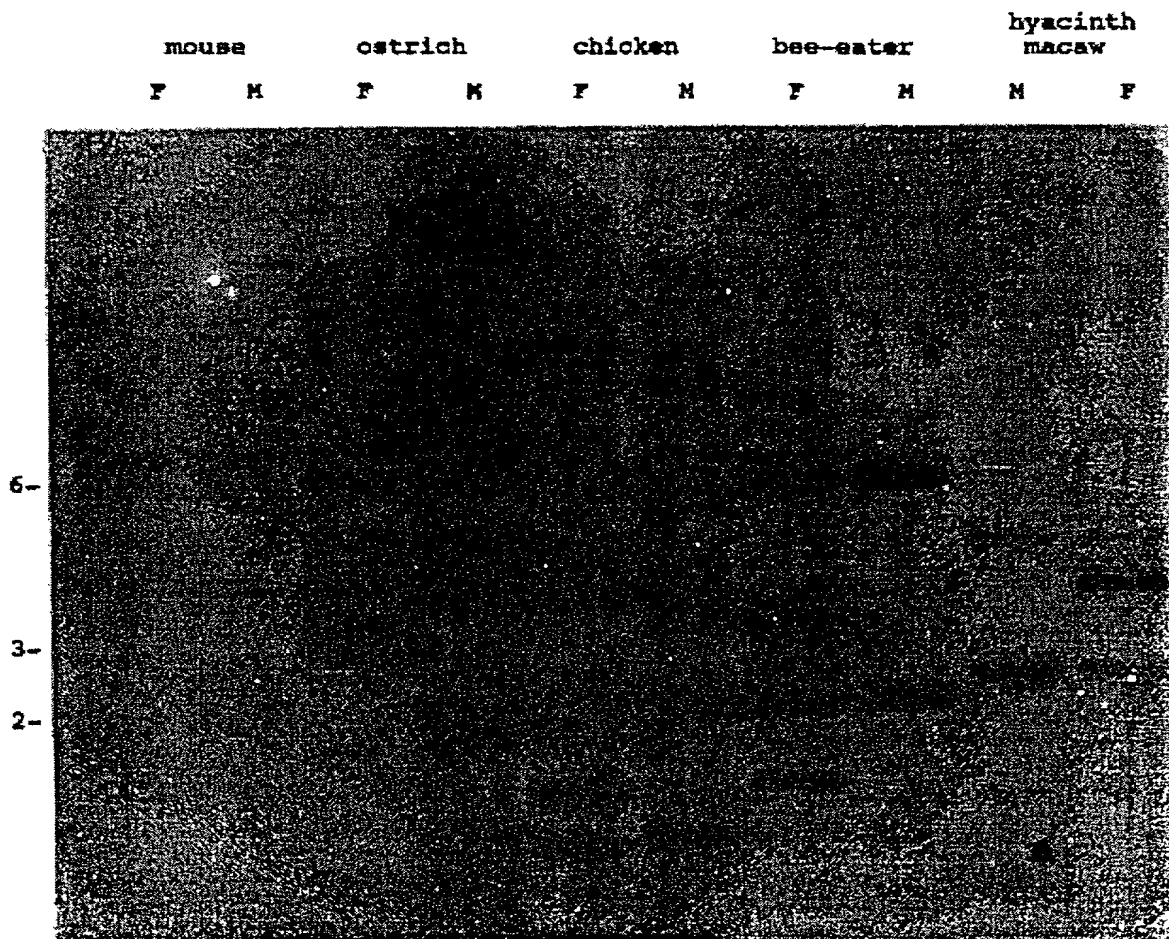


Figure 13.



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Figure 14.

MOUSE	CHD1	AGA TAT TCT GGA TCT GAT AGT GAT TCA ATC TCG GAA
CHICKEN	CHD-1A	--- --- --- --- --- --- --- -C -C --- A-A ---
SPIX	CHD-1A	--- --- --- --- --- --- --- C -C --- --- ---
CHICKEN	CHD-W	--- --- --- --- --- --- --- -C --- -A ---
SPIX	CHD-W	--- --- --- --- --- --- --- C -C --- -A ---
HYACINTH	CHD-W	--- --- --- --- --- --- --- C -C --- -A ---
P1		A TAT TCT GGA TCT GAT AGT GAT TC
P3		AGA TAT TCC GGA TCT GAT AGT GA
MOUSE	CHD1	AGG AAA <u>CGG</u> <u>CCG</u> AAG AAA CGT GGG CGA CCC CGC ACT
CHICKEN	CHD-1A	--A --- --- --A --A --G --- --A A-- --T --A --C
SPIX	CHD-1A	--- --- --- --A --A --G --- --A A-- --A --A ---
CHICKEN	CHD-W	--A --- --A --A --A --- --- --A --- --A --A ---
SPIX	CHD-W	--A --- --A --A --GA --- --- --A --- --A --A ---
HYACINTH	CHD-W	--A --- --A --A --GA --- --- --A --- --A --A ---
MOUSE	CHD1	ATC CCT CGG GAG AAT ATT AAA GGA TTT AGT GAT GCG GAG
CHICKEN	CHD-1A	--T --- --A --A --- --- --- --- --- --- --A ---
SPIX	CHD-1A	--T --- --A --A --- --A --- --- --- --- --- --A ---
CHICKEN	CHD-W	--T --C --T --A --C --- --- --- --- --- --A ---
SPIX	CHD-W	--T --- --T --A --- --- --- --- --- --- --A ---
P2		TTT CCT AAA TCG CTA CGT CT
HYACINTH	CHD-W	ATT AGG CGG T

Figure 15.

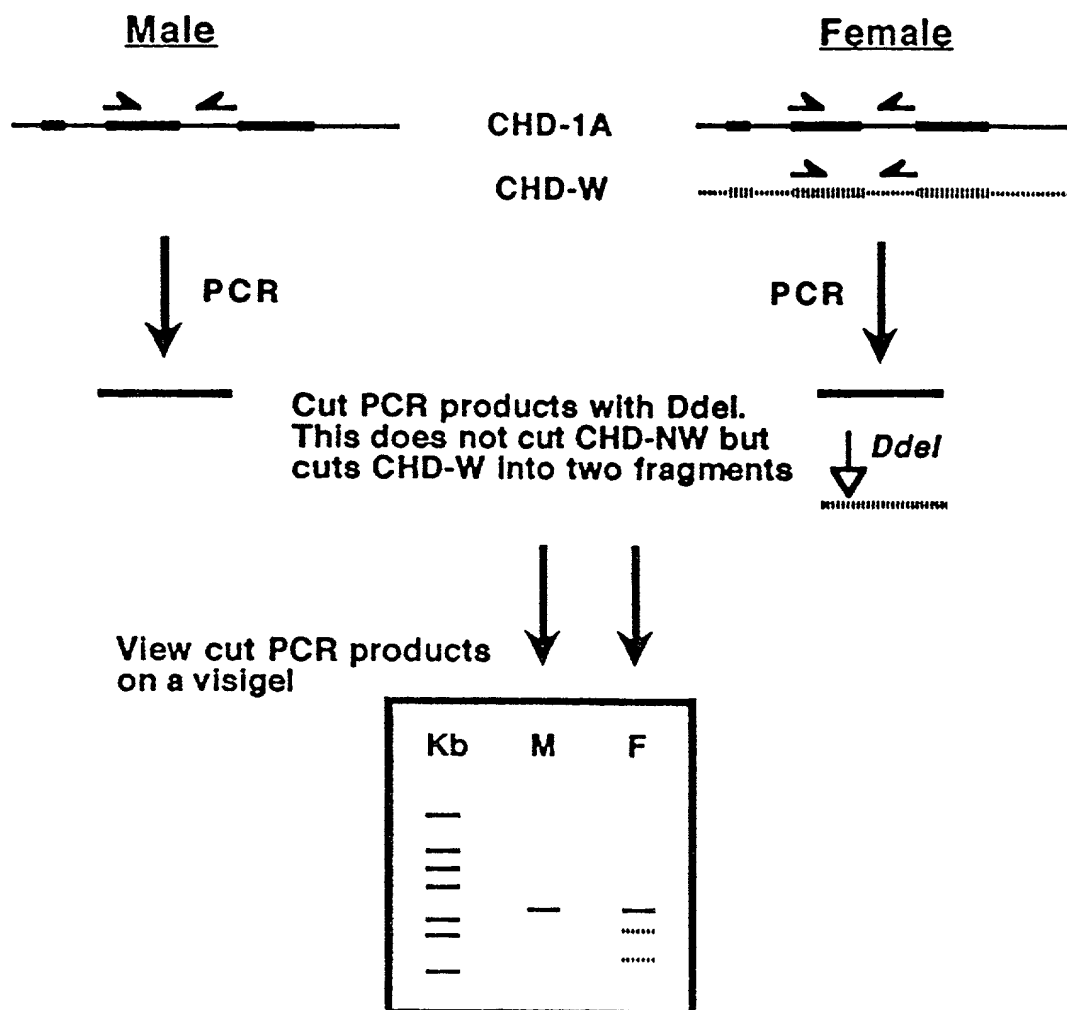




Figure 16.

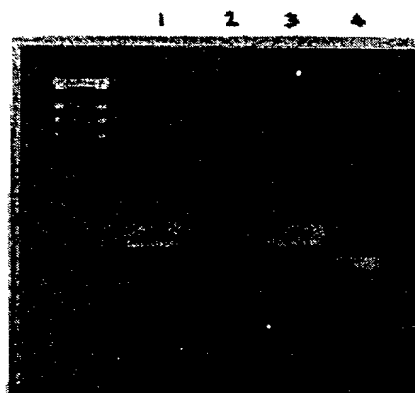
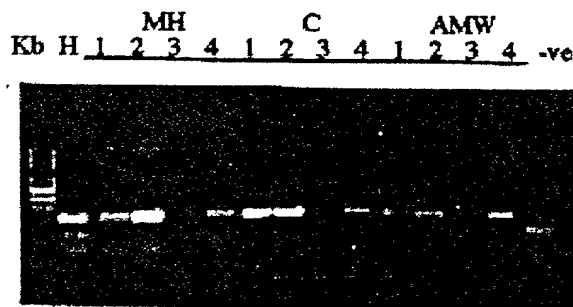


Figure 17.



## DECLARATION AND POWER OF ATTORNEY FOR U.S. PATENT APPLICATIONS

( ) Original ( ) Supplemental ( ) Substitute ( ) PCT ( ) DESIGN

As a below named inventor, I hereby declare that: my residence, post office address and citizenship are as stated below next to my name; that I verily believe that I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural inventors are named below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

Title: AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN BIRDS

which is described and claimed in:

( ) the attached specification, or  
 ( ) the specification in the application Serial No. \_\_\_\_\_ filed \_\_\_\_\_;  
 and with amendments through \_\_\_\_\_ (if applicable),  
 (X) the specification in International Application No. PCT/GB96/01341, filed  
 5 June 1996, and as amended on 13 June 1997 (if applicable).

I hereby state that I have reviewed and understand the content of the above-identified specification, including the claims, as amended by any amendment(s) referred to above.

I acknowledge my duty to disclose information of which I am aware which is material to the examination of this application in accordance with Title 37, Code of Federal Regulations, §1.56(a).

I hereby claim foreign priority benefits under Title 35, United States Code, §119 (and §172 if this application is for a Design) of any foreign application(s) for patent or inventor's certificate listed below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of the application on which priority is claimed:

COUNTRY	APPLICATION NO.	DATE OF FILING	PRIORITY CLAIMED
GB	9511439.3	6 June 1995	(X) YES ( ) NO
			( ) YES ( ) NO
			( ) YES ( ) NO
			( ) YES ( ) NO
			( ) YES ( ) NO
			( ) YES ( ) NO

I hereby claim the benefit under Title 35, United States Code, §120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, §1.56(a) which occurred between the filing date of the prior application and the national or PCT international filing date of this application:

SERIAL NO.	U.S. FILING DATE	STATUS
		( ) Patented ( ) Pending ( ) Abandoned
		( ) Patented ( ) Pending ( ) Abandoned
		( ) Patented ( ) Pending ( ) Abandoned

And I hereby appoint V. M. Creedon, Reg. No. 17111, John T. Miller, Reg. No. 21120, John T. Fedigan, Reg. No. 24347, Michael R. Davis, Reg. No. 25134, Matthew M. Jacob, Reg. No. 25154, Jeffrey Noltan, Reg. No. 25408, and Henry M. Zykorie, Reg. No. 27477, who together constitute the firm of WENDEROTH, LIND & PONACK, jointly and severally, attorneys to prosecute this application and to transact all business in the U.S. Patent and Trademark Office connected therewith.

I hereby authorize the U.S. attorneys named herein to accept and follow instructions from Stevens, Hewlett & Perkins as to any action to be taken in the U.S. Patent and Trademark Office regarding this application without direct communication between the U.S. attorneys and myself. In the event of a change in the persons from whom instructions may be taken, the U.S. attorneys named herein will be so notified by me.

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	RESIDENCE & CITIZENSHIP	CITY	STATE OR COUNTRY	COUNTRY OF CITIZENSHIP
	POST OFFICE ADDRESS	ADDRESS	CITY	STATE OR COUNTRY ZIP CODE
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	RESIDENCE & CITIZENSHIP	CITY	STATE OR COUNTRY	COUNTRY OF CITIZENSHIP
	POST OFFICE ADDRESS	ADDRESS	CITY	STATE OR COUNTRY ZIP CODE
6th INVENTOR	FULL NAME OF 6TH INVENTOR	FAMILY NAME	FIRST GIVEN NAME	SECOND GIVEN NAME
	RESIDENCE & CITIZENSHIP	CITY	STATE OR COUNTRY	COUNTRY OF CITIZENSHIP
	POST OFFICE ADDRESS	ADDRESS	CITY	STATE OR COUNTRY ZIP CODE

I further declare that all statements made herein of my own knowledge are true, and that all statements on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

1st Inventor R. Griffiths Date 19/1/98  
 2nd Inventor Bela Tiwari Date 21/1/98  
 3rd Inventor TIWARI, BELA Date \_\_\_\_\_  
 4th Inventor \_\_\_\_\_ Date \_\_\_\_\_  
 5th Inventor \_\_\_\_\_ Date \_\_\_\_\_  
 6th Inventor \_\_\_\_\_ Date \_\_\_\_\_

The above application may be more particularly identified as follows:

U. S. Application Serial No. \_\_\_\_\_, Filing Date \_\_\_\_\_  
 Applicant Reference Number \_\_\_\_\_, Atty Docket No. \_\_\_\_\_  
 Title of Invention \_\_\_\_\_